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(54) Title: SYSTEM FOR *IN VITRO* TRANSPOSITION USING MODIFIED TN5 TRANSPOSASE

(57) Abstract

A system for *in vitro* transposition includes a donor DNA that includes a transposable element flanked by a pair of bacterial transposon Tn5 outside end repeat sequences, a target DNA into which the transposable element can transpose, and a modified Tn5 transposase having higher binding avidity to the outside end repeat sequences and being less likely to assume an inactive multimer form than wild type Tn5 transposase.

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SYSTEM FOR *IN VITRO* TRANSPOSITION USING MODIFIED TN5 TRANSPOSASE

CROSS-REFERENCE TO RELATED APPLICATION

This patent application is a continuation-in-part of a patent application entitled "System for *In Vitro* Transposition," filed March 11, 1997, for which no serial number has yet been accorded. Applicants have petitioned for a filing date of September 9, 1996 to be accorded to the parent application.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

Not applicable.

BACKGROUND OF THE INVENTION

The present invention relates generally to the field of transposable nucleic acid and, more particularly to production and use of a modified transposase enzyme in a system for introducing genetic changes to nucleic acid.

Transposable genetic elements are DNA sequences, found in a wide variety of prokaryotic and eukaryotic organisms, that can move or transpose from one position to another position in a genome. *In vivo*, intra-chromosomal transpositions as well as transpositions between chromosomal and non-chromosomal genetic material are known. In several systems, transposition is known to be under the control of a transposase enzyme that is typically encoded by the transposable element. The genetic structures and transposition mechanisms of various transposable elements are summarized, for example, in "Transposable Genetic Elements" in "The Encyclopedia of Molecular Biology," Kendrew and Lawrence, Eds., Blackwell Science, Ltd., Oxford (1994), incorporated herein by reference.

In vitro transposition systems that utilize the particular transposable elements of bacteriophage Mu and bacterial transposon Tn*10* have been described, by the research groups of

Kiyoshi Mizuuchi and Nancy Kleckner, respectively.

The bacteriophage Mu system was first described by Mizuuchi, K., "*In Vitro* Transposition of Bacteria Phage Mu: A Biochemical Approach to a Novel Replication Reaction," Cell:785-794 (1983) and Craigie, R. et al., "A Defined System for the DNA Strand-Transfer Reaction at the Initiation of Bacteriophage Mu Transposition: Protein and DNA Substrate Requirements," P.N.A.S. U.S.A. 82:7570-7574 (1985). The DNA donor substrate (mini-Mu) for Mu *in vitro* reaction normally requires six Mu transposase binding sites (three of about 30 bp at each end) and an enhancer sequence located about 1 kb from the left end. The donor plasmid must be supercoiled. Proteins required are Mu-encoded A and B proteins and host-encoded HU and IHF proteins. Lavoie, B.D, and G. Chaconas, "Transposition of phage Mu DNA," Curr. Topics Microbiol. Immunol. 204:83-99 (1995). The Mu-based system is disfavored for *in vitro* transposition system applications because the Mu termini are complex and sophisticated and because transposition requires additional proteins above and beyond the transposase.

The Tn*10* system was described by Morisato, D. and N. Kleckner, "Tn*10* Transposition and Circle Formation *in vitro*," Cell 51:101-111 (1987) and by Benjamin, H. W. and N. Kleckner, "Excision Of Tn*10* from the Donor Site During Transposition Occurs By Flush Double-Strand Cleavages at the Transposon Termini," P.N.A.S. U.S.A. 89:4648-4652 (1992). The Tn*10* system involves the a supercoiled circular DNA molecule carrying the transposable element (or a linear DNA molecule plus *E. coli* IHF protein). The transposable element is defined by complex 42 bp terminal sequences with IHF binding site adjacent to the inverted repeat. In fact, even longer (81 bp) ends of Tn*10* were used in reported experiments. Sakai, J. et al., "Identification and Characterization of Pre-Cleavage Synaptic Complex that is an Early Intermediate in Tn*10* transposition," E.M.B.O. J. 14:4374-4383 (1995). In the Tn*10* system, chemical treatment of the transposase protein is essential to support active transposition. In addition, the termini of the Tn*10* element limit its utility in a generalized *in vitro*

transposition system.

Both the Mu- and Tn*10*-based *in vitro* transposition systems are further limited in that they are active only on covalently closed circular, supercoiled DNA targets. What is desired is a more broadly applicable *in vitro* transposition system that utilizes shorter, more well defined termini and which is active on target DNA of any structure (linear, relaxed circular, and supercoiled circular DNA).

BRIEF SUMMARY OF THE INVENTION

The present invention is summarized in that an *in vitro* transposition system comprises a preparation of a suitably modified transposase of bacterial transposon Tn*5*, a donor DNA molecule that includes a transposable element, a target DNA molecule into which the transposable element can transpose, all provided in a suitable reaction buffer.

The transposable element of the donor DNA molecule is characterized as a transposable DNA sequence of interest, the DNA sequence of interest being flanked at its 5'- and 3'-ends by short repeat sequences that are acted upon *in trans* by Tn*5* transposase.

The invention is further summarized in that the suitably modified transposase enzyme comprises two classes of differences from wild type Tn*5* transposase, where each class has a separate measurable effect upon the overall transposition activity of the enzyme and where a greater effect is observed when both modifications are present. The suitably modified enzyme both (1) binds to the repeat sequences of the donor DNA with greater avidity than wild type Tn*5* transposase ("class (1) mutation") and (2) is less likely than the wild type protein to assume an inactive multimeric form ("class (2) mutation"). A suitably modified Tn*5* transposase of the present invention that contains both class (1) and class (2) modifications induces at least about 100-fold (±10%) more transposition than the wild type enzyme, when tested in combination in an *in vivo* conjugation assay as described by Weinreich, M.D., "Evidence that the *cis* Preference of the Tn*5* Transposase is Caused by

Nonproductive Multimerization," Genes and Development 8:2363-2374 (1994), incorporated herein by reference. Under optimal conditions, transposition using the modified transposase may be higher. A modified transposase containing only a class (1) mutation binds to the repeat sequences with sufficiently greater avidity than the wild type Tn5 transposase that such a Tn5 transposase induces about 5- to 50-fold more transposition than the wild type enzyme, when measured *in vivo*. A modified transposase containing only a class (2) mutation is sufficiently less likely than the wild type Tn5 transposase to assume the multimeric form that such a Tn5 transposase also induces about 5- to 50-fold more transposition than the wild type enzyme, when measured *in vivo*.

In another aspect, the invention is summarized in that a method for transposing the transposable element from the donor DNA into the target DNA *in vitro* includes the steps of mixing together the suitably modified Tn5 transposase protein, the donor DNA, and the target DNA in a suitable reaction buffer, allowing the enzyme to bind to the flanking repeat sequences of the donor DNA at a temperature greater than 0°C, but no higher than about 28°C, and then raising the temperature to physiological temperature (about 37°C) whereupon cleavage and strand transfer can occur.

It is an object of the present invention to provide a useful *in vitro* transposition system having few structural requirements and high efficiency.

It is another object of the present invention to provide a method that can be broadly applied in various ways, such as to create absolute defective mutants, to provide selective markers to target DNA, to provide portable regions of homology to a target DNA, to facilitate insertion of specialized DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequencing, to facilitate production of genetic fusions for gene expression studies and protein domain mapping, as well as to bring together other desired combinations of DNA sequences (combinatorial genetics).

It is a feature of the present invention that the modified

transposase enzyme binds more tightly to DNA than does wild type Tn*5* transposase.

It is an advantage of the present invention that the modified transposase facilitates *in vitro* transposition reaction rates of at least about 100-fold higher than can be achieved using wild type transposase (as measured *in vivo*). It is noted that the wild-type Tn*5* transposase shows no detectable *in vitro* activity in the system of the present invention. Thus, while it is difficult to calculate an upper limit to the increase in activity, it is clear that hundreds, if not thousands, of colonies are observed when the products of *in vitro* transposition are assayed *in vivo*.

It is another advantage of the present invention that *in vitro* transposition using this system can utilize donor DNA and target DNA that is circular or linear.

It is yet another advantage of the present invention that *in vitro* transposition using this system requires no outside high energy source and no other protein other than the modified transposase.

Other objects, features, and advantages of the present invention will become apparent upon consideration of the following detailed description.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

Fig. 1 depicts test plasmid pRZTL1, used herein to demonstrate transposition *in vitro* of a transposable element located between a pair of Tn*5* outside end termini. Plasmid pRZTL1 is also shown and described in SEQ ID NO:3.

Fig. 2 depicts an electrophoretic analysis of plasmid pRZTL1 before and after *in vitro* transposition. Data obtained using both circular and linear plasmid substrates are shown.

Fig. 3 is an electrophoretic analysis of plasmid pRZTL1 after *in vitro* transposition, including further analysis of the molecular species obtained using circular and linear plasmid substrates.

Fig. 4 shows plasmids pRZ1496, pRZ5451 and pRZTL1, which are detailed in the specification.

Fig. 5 shows a plot of papillae per colony over time for various mutant OE sequences tested *in vivo* against EK54/MA56 transposase.

Fig. 6 shows a plot of papillae per colony over time for various mutant OE sequences with a smaller Y-axis than is shown in Fig. 5 tested against EK54/MA56 transposase.

Fig. 7 shows a plot of papillae per colony over time for various mutant OE sequences tested against MA56 Tn5 transposase.

Fig. 8 shows *in vivo* transposition using two preferred mutants, tested against MA56 and EK54/MA56 transposase.

DETAILED DESCRIPTION OF THE INVENTION

It will be appreciated that this technique provides a simple, *in vitro* system for introducing any transposable element from a donor DNA into a target DNA. It is generally accepted and understood that Tn5 transposition requires only a pair of OE termini, located to either side of the transposable element. These OE termini are generally thought to be 18 or 19 bases in length and are inverted repeats relative to one another. Johnson, R. C., and W. S. Reznikoff, Nature 304:280 (1983), incorporated herein by reference. The Tn5 inverted repeat sequences, which are referred to as "termini" even though they need not be at the termini of the donor DNA molecule, are well known and understood.

Apart from the need to flank the desired transposable element with standard Tn5 outside end ("OE") termini, few other requirements on either the donor DNA or the target DNA are envisioned. It is thought that Tn5 has few, if any, preferences for insertion sites, so it is possible to use the system to introduce desired sequences at random into target DNA. Therefore, it is believed that this method, employing the modified transposase described herein and a simple donor DNA, is broadly applicable to introduce changes into any target DNA, without regard to its nucleotide sequence. It will, thus, be applied to many problems of interest to those skilled in the art of molecular biology.

In the method, the modified transposase protein is combined in a suitable reaction buffer with the donor DNA and the target DNA. A suitable reaction buffer permits the transposition reaction to occur. A preferred, but not necessarily optimized, buffer contains spermidine to condense the DNA, glutamate, and magnesium, as well as a detergent, which is preferably 3-[(3-cholamidopropyl) dimethyl-ammonio]-1-propane sulfonate ("CHAPS"). The mixture can be incubated at a temperature greater than 0°C and as high as about 28°C to facilitate binding of the enzyme to the OE termini. Under the buffer conditions used by the inventors in the Examples, a pretreatment temperature of 30°C was not adequate. A preferred temperature range is between 16°C and 28°C. A most preferred pretreatment temperature is about 20°C. Under different buffer conditions, however, it may be possible to use other below-physiological temperatures for the binding step. After a short pretreatment period of time (which has not been optimized, but which may be as little as 30 minutes or as much as 2 hours, and is typically 1 hour), the reaction mixture is diluted with 2 volumes of a suitable reaction buffer and shifted to physiological conditions for several more hours (say 2-3 hours) to permit cleavage and strand transfer to occur. A temperature of 37°C, or thereabouts, is adequate. After about 3 hours, the rate of transposition decreases markedly. The reaction can be stopped by phenol-chloroform extraction and can then be desalted by ethanol precipitation.

When the DNA has been purified using conventional purification tools, it is possible to employ simpler reaction conditions in the *in vitro* transposition method. DNA of sufficiently high purity can be prepared by passing the DNA preparation through a resin of the type now commonly used in the molecular biology laboratory, such as the Qiagen resin of the Qiagen plasmid purification kit (Catalog No. 12162). When such higher quality DNA is employed, CHAPS can be omitted from the reaction buffer. When CHAPS is eliminated from the reaction buffer, the reactants need not be diluted in the manner described above. Also, the low temperature incubation

step noted above can be eliminated in favor of a single incubation for cleavage and strand transfer at physiological conditions. A three hour incubation at 37°C is sufficient.

Following the reaction and subsequent extraction steps, transposition can be assayed by introducing the nucleic acid reaction products into suitable bacterial host cells (e.g., *E. coli* K-12 DH5α cells (recA$^-$); commercially available from Life Technologies (Gibco-BRL)) preferably by electroporation, described by Dower et al., Nuc. Acids. Res. 16:6127 (1988), and monitoring for evidence of transposition, as is described elsewhere herein.

Those persons skilled in the art will appreciate that apart from the changes noted herein, the transposition reaction can proceed under much the same conditions as would be found in an *in vivo* reaction. Yet, the modified transposase described herein so increases the level of transposition activity that it is now possible to carry out this reaction *in vitro* where this has not previously been possible. The rates of reaction are even greater when the modified transposase is coupled with an optimized buffer and temperature conditions noted herein.

In another aspect, the present invention is a preparation of a modified Tn*5* transposase enzyme that differs from wild type Tn*5* transposase in that it (1) binds to the repeat sequences of the donor DNA with greater avidity than wild type Tn*5* transposase and (2) is less likely than the wild type protein to assume an inactive multimeric form. An enzyme having these requirements can be obtained from a bacterial host cell containing an expressible gene for the modified enzyme that is under the control of a promoter active in the host cell. Genetic material that encodes the modified Tn*5* transposase can be introduced (e.g., by electroporation) into suitable bacterial host cells capable of supporting expression of the genetic material. Known methods for overproducing and preparing other Tn*5* transposase mutants are suitably employed. For example, Weinreich, M. D., et al., *supra*, describes a suitable method for overproducing a Tn*5* transposase. A second method for purifying Tn*5* transposase was described in de la

Cruz, N. B., et al., "Characterization of the Tn5 Transposase and Inhibitor Proteins: A Model for the Inhibition of Transposition," J. Bact. 175:6932-6938 (1993), also incorporated herein by reference. It is noted that induction can be carried out at temperatures below 37°C, which is the temperature used by de la Cruz, et al. Temperatures at least in the range of 33 to 37°C are suitable. The inventors have determined that the method for preparing the modified transposase of the present invention is not critical to success of the method, as various preparation strategies have been used with equal success.

Alternatively, the protein can be chemically synthesized, in a manner known to the art, using the amino acid sequence attached hereto as SEQ ID NO:2 as a guide. It is also possible to prepare a genetic construct that encodes the modified protein (and associated transcription and translation signals) by using standard recombinant DNA methods familiar to molecular biologists. The genetic material useful for preparing such constructs can be obtained from existing Tn5 constructs, or can be prepared using known methods for introducing mutations into genetic material (e.g., random mutagenesis PCR or site-directed mutagenesis) or some combination of both methods. The genetic sequence that encodes the protein shown in SEQ ID NO:2 is set forth in SEQ ID NO:1.

The nucleic acid and amino acid sequence of wild type Tn5 transposase are known and published. N.C.B.I. Accession Number U00004 L19385, incorporated herein by reference.

In a preferred embodiment, the improved avidity of the modified transposase for the repeat sequences for OE termini (class (1) mutation) can be achieved by providing a lysine residue at amino acid 54, which is glutamic acid in wild type Tn5 transposase. The mutation strongly alters the preference of the transposase for OE termini, as opposed to inside end ("IE") termini. The higher binding of this mutation, known as EK54, to OE termini results in a transposition rate that is about 10-fold higher than is seen with wild type transposase. A similar change at position 54 to valine (mutant EV54) also

results in somewhat increased binding/transposition for OE termini, as does a threonine-to-proline change at position 47 (mutant TP47; about 10-fold higher). It is believed that other, comparable transposase mutations (in one or more amino acids) that increase binding avidity for OE termini may also be obtained which would function as well or better in the *in vitro* assay described herein.

One of ordinary skill will also appreciate that changes to the nucleotide sequences of the short repeat sequences of the donor DNA may coordinate with other mutation(s) in or near the binding region of the transposase enzyme to achieve the same increased binding effect, and the resulting 5- to 50-fold increase in transposition rate. Thus, while the applicants have exemplified one case of a mutation that improves binding of the exemplified transposase, it will be understood that other mutations in the transposase, or in the short repeat sequences, or in both, will also yield transposases that fall within the scope and spirit of the present invention. A suitable method for determining the relative avidity for Tn*5* OE termini has been published by Jilk, R. A., et al., "The Organization of the Outside end of Transposon Tn5," J. Bact. 178:1671-79 (1996).

The transposase of the present invention is also less likely than the wild type protein to assume an inactive multimeric form. In the preferred embodiment, that class (2) mutation from wild type can be achieved by modifying amino acid 372 (leucine) of wild type Tn*5* transposase to a proline (and, likewise by modifying the corresponding DNA to encode proline). This mutation, referred to as LP372, has previously been characterized as a mutation in the dimerization region of the transposase. Weinreich, et al., *supra*. It was noted by Weinreich et al. that this mutation at position 372 maps to a region shown previously to be critical for interaction with an inhibitor of Tn*5* transposition. The inhibitor is a protein encoded by the same gene that encodes the transposase, but which is truncated at the N-terminal end of the protein, relative to the transposase. The approach of Weinreich et al.

for determining the extent to which multimers are formed is suitable for determining whether a mutation falls within the scope of this element.

It is thought that when wild type Tn5 transposase multimerizes, its activity *in trans* is reduced. Presumably, a mutation in the dimerization region reduces or prevents multimerization, thereby reducing inhibitory activity and leading to levels of transposition 5- to 50-fold higher than are seen with the wild type transposase. The LP372 mutation achieves about 10-fold higher transposition levels than wild type. Likewise, other mutations (including mutations at a one or more amino acid) that reduce the ability of the transposase to multimerize would also function in the same manner as the single mutation at position 372, and would also be suitable in a transposase of the present invention. It may also be possible to reduce the ability of a Tn5 transposase to multimerize without altering the wild type sequence in the so-called dimerization region, for example by adding into the system another protein or non-protein agent that blocks the dimerization site. Alternatively, the dimerization region could be removed entirely from the transposase protein.

As was noted above, the inhibitor protein, encoded in partially overlapping sequence with the transposase, can interfere with transposase activity. As such, it is desired that the amount of inhibitor protein be reduced over the amount observed in wild type *in vivo*. For the present assay, the transposase is used in purified form, and it may be possible to separate the transposase from the inhibitor (for example, according to differences in size) before use. However, it is also possible to genetically eliminate the possibility of having any contaminating inhibitor protein present by removing its start codon from the gene that encodes the transposase.

An AUG in the wild type Tn5 transposase gene that encodes methionine at transposase amino acid 56 is the first codon of the inhibitor protein. However, it has already been shown that replacement of the methionine at position 56 has no apparent effect upon the transposase activity, but at the same time

prevents translation of the inhibitor protein, thus resulting in a somewhat higher transposition rate. Weigand, T. W. and W. S. Reznikoff, "Characterization of Two Hypertransposing Tn5 Mutants," J. Bact. 174:1229-1239 (1992), incorporated herein by reference. In particular, the present inventors have replaced the methionine with an alanine in the preferred embodiment (and have replaced the methionine-encoding AUG codon with an alanine-encoding GCC). A preferred transposase of the present invention therefore includes an amino acid other than methionine at amino acid position 56, although this change can be considered merely technically advantageous (since it ensures the absence of the inhibitor from the *in vitro* system) and not essential to the invention (since other means can be used to eliminate the inhibitor protein from the *in vitro* system).

The most preferred transposase amino acid sequence known to the inventors differs from the wild type at amino acid positions 54, 56, and 372. The mutations at positions 54 and 372 separately contribute approximately a 10-fold increase to the rate of transposition reaction *in vivo*. When the mutations are combined using standard recombinant techniques into a single molecule containing both classes of mutations, reaction rates of at least about 100-fold higher than can be achieved using wild type transposase are observed when the products of the *in vitro* system are tested *in vivo*. The mutation at position 56 does not directly affect the transposase activity.

Other mutants from wild type that are contemplated to be likely to contribute to high transposase activity *in vitro* include, but are not limited to glutaminic acid-to-lysine at position 110, and glutamic acid to lysine at position 345.

It is, of course, understood that other changes apart from these noted positions can be made to the modified transposase (or to a construct encoding the modified transposase) without adversely affecting the transposase activity. For example, it is well understood that a construct encoding such a transposase could include changes in the third position of codons such that the encoded amino acid does not differ from that described herein. In addition, certain codon changes have little or no

functional effect upon the transposition activity of the encoded protein. Finally, other changes may be introduced which provide yet higher transposition activity in the encoded protein. It is also specifically envisioned that combinations of mutations can be combined to encode a modified transposase having even higher transposition activity than has been exemplified herein. All of these changes are within the scope of the present invention. It is noted, however, that a modified transposase containing the EK110 and EK345 mutations (both described by Weigand and Reznikoff, *supra*, had lower transposase activity than a transposase containing either mutation alone.

After the enzyme is prepared and purified, as described *supra*, it can be used in the *in vitro* transposition reaction described above to introduce any desired transposable element from a donor DNA into a target DNA. The donor DNA can be circular or can be linear. If the donor DNA is linear, it is preferred that the repeat sequences flanking the transposable element should not be at the termini of the linear fragment but should rather include some DNA upstream and downstream from the region flanked by the repeat sequences.

As was noted above, Tn*5* transposition requires a pair of eighteen or nineteen base long termini. The wild type Tn*5* outside end (OE) sequence (5'-CTGACTCTTATACACAAGT-3') (SEQ ID NO: 7) has been described. It has been discovered that a transposase-catalyzed *in vitro* transposition frequency at least as high as that of wild type OE is achieved if the termini in a construct include bases ATA at positions 10, 11, and 12, respectively, as well as the nucleotides in common between wild type OE and IE (e.g., at positions 1-3, 5-9, 13, 14, 16, and optionally 19). The nucleotides at positions 4, 15, 17, and 18 can correspond to the nucleotides found at those positions in either wild type OE or wild type IE. It is noted that the transposition frequency can be enhanced over that of wild type OE if the nucleotide at position 4 is a T. The importance of these particular bases to transposition frequency has not previously been identified.

It is noted that these changes are not intended to encompass every desirable modification to OE. As is described elsewhere herein, these attributes of acceptable termini modifications were identified by screening mutants having randomized differences between IE and OE termini. While the presence in the termini of certain nucleotides is shown herein to be advantageous, other desirable terminal sequences may yet be obtained by screening a larger array of degenerate mutants that include changes at positions other than those tested herein as well as mutants containing nucleotides not tested in the described screening. In addition, it is clear to one skilled in the art that if a different transposase is used, it may still be possible to select other variant termini, more compatible with that particular transposase.

Among the mutants shown to be desirable and within the scope of the invention are two hyperactive mutant OE sequences that were identified *in vivo*. Although presented here as single stranded sequences, in fact, the wild type and mutant OE sequences include complementary second strands. The first hyperactive mutant, 5'-CTGTCTCTTATACACATCT-3' (SEQ ID NO: 8), differs from the wild type OE sequence at positions 4, 17, and 18, counting from the 5' end, but retains ATA at positions 10-12. The second, 5'-CTGTCTCTTATACAGATCT-3' (SEQ ID NO: 9), differs from the wild type OE sequence at positions 4, 15, 17, and 18, but also retains ATA at positions 10-12. These two hyperactive mutant OE sequences differ from one another only at position 15, where either G or C is present. OE-like activity (or higher activity) is observed in a mutant sequence when it contains ATA at positions 10, 11 and 12. It may be possible to reduce the length of the OE sequence from 19 to 18 nucleotide pairs with little or no effect.

When one of the identified hyperactive mutant OE sequences flanks a substrate DNA, the *in vivo* transposition frequency of EK54/MA56 transposase is increased approximately 40-60 fold over the frequency that is observed when wild type OE termini flank the transposable DNA. The EK54/MA56 transposase is already known to have an *in vivo* transposition frequency

approximately an 8-10 fold higher than wild type transposase, using wild type OE termini. Tn*5* transposase having the EK54/MA56 mutation is known to bind with greater avidity to OE and with lesser avidity to the Tn*5* inside ends (IE) than wild type transposase.

A suitable mutant terminus in a construct for use in the assays of the present invention is characterized biologically as yielding more papillae per colony in a comparable time, say 68 hours, than is observed in colonies harboring wild type OE in a comparable plasmid. Wild type OE can yield about 100 papillae per colony when measured 68 hours after plating in a papillation assay using EK54/MA56 transposase, as is described elsewhere herein. A preferred mutant would yield between about 200 and 3000 papillae per colony, and a more preferred mutant between about 1000 and 3000 papillae per colony, when measured in the same assay and time frame. A most preferred mutant would yield between about 2000 and 3000 papillae per colony when assayed under the same conditions. Papillation levels may be even greater than 3000 per colony, although it is difficult to quantitate at such levels.

Transposition frequency is also substantially enhanced in the *in vitro* transposition assay of the present invention when substrate DNA is flanked by a preferred mutant OE sequence and a most preferred mutant transposase (comprising EK54/MA56/LP372 mutations) is used. Under those conditions, essentially all of the substrate DNA is converted into transposition products.

The rate of *in vitro* transposition observed using the hyperactive termini is sufficiently high that, in the experience of the inventors, there is no need to select for transposition events. All colonies selected at random after transformation for further study have shown evidence of transposition events.

This advance can represent a significant savings in time and laboratory effort. For example, it is particularly advantageous to be able to improve *in vitro* transposition frequency by modifying DNA rather than by modifying the transposase because as transposase activity increases in host

cells, there is an increased likelihood that cells containing the transposase are killed during growth as a result of aberrant DNA transpositions. In contrast, DNA of interest containing the modified OE termini can be grown in sources completely separate from the transposase, thus not putting the host cells at risk.

Without intending to limit the scope of this aspect of this invention, it is apparent that the tested hyperactive termini do not bind with greater avidity to the transposase than do wild type OE termini. Thus, the higher transposition frequency brought about by the hyperactive termini is not due to enhanced binding to transposase.

The transposable element between the termini can include any desired nucleotide sequence. The length of the transposable element between the termini should be at least about 50 base pairs, although smaller inserts may work. No upper limit to the insert size is known. However, it is known that a donor DNA portion of about 300 nucleotides in length can function well. By way of non-limiting examples, the transposable element can include a coding region that encodes a detectable or selectable protein, with or without associated regulatory elements such as promoter, terminator, or the like.

If the element includes such a detectable or selectable coding region without a promoter, it will be possible to identify and map promoters in the target DNA that are uncovered by transposition of the coding region into a position downstream thereof, followed by analysis of the nucleic acid sequences upstream from the transposition site.

Likewise, the element can include a primer binding site that can be transposed into the target DNA, to facilitate sequencing methods or other methods that rely upon the use of primers distributed throughout the target genetic material. Similarly, the method can be used to introduce a desired restriction enzyme site or polylinker, or a site suitable for another type of recombination, such as a cre-lox, into the target.

The invention can be better understood upon consideration

of the following examples which are intended to be exemplary and not limiting on the invention.

EXAMPLES

To obtain the transposase modified at position 54, the first third of the coding region from an existing DNA clone that encodes the Tn*5* transposase but not the inhibitor protein (MA56) was mutagenized according to known methods and DNA fragments containing the mutagenized portion were cloned to produce a library of plasmid clones containing a full length transposase gene. The clones making up the library were transformed into *E. coli* K-12 strain MDW320 bacteria which were plated and grown into colonies. Transposable elements provided in the bacteria on a separate plasmid contained a defective lacZ gene. The separate plasmid, pOXgen386, was described by Weinreich, M. et al., "A functional analysis of the Tn*5* Transposase: Identification of Domains Required for DNA Binding and Dimerization," J. Mol. Biol. 241:166-177 (1993), incorporated herein by reference. Colonies having elevated transposase activity were selected by screening for blue (LacZ) spots in white colonies grown in the presence of X-gal. This papillation assay was described by Weinreich, et al. (1993), *supra*. The 5'-most third of Tn*5* transposase genes from such colonies were sequenced to determine whether a mutation was responsible for the increase in transposase activity. It was determined that a mutation at position 54 to lysine (K) correlated well with the increase in transposase activity. Plasmid pRZ5412-EK54 contains lysine at position 54 as well as the described alanine at position 56.

The fragment containing the LP372 mutation was isolated from pRZ4870 (Weinreich et al (1994)) using restriction enzymes NheI and BglII, and were ligated into NheI-BglII cut pRZ5412-EK54 to form a recombinant gene having the mutations at positions 54, 56 and 372, as described herein and shown in SEQ ID NO:1. The gene was tested and shown to have at least about a one hundred fold increase in activity relative to wild type Tn*5* transposase. Each of the mutants at positions 54 and 372

alone had about a 10-fold increase in transposase activity.

The modified transposase protein encoded by the triple-mutant recombinant gene was transferred into commercial T7 expression vector pET-21D (commercially available from Novagen, Madison, WI) by inserting a BspHI/SalI fragment into NhoI/XhoI fragment of the pET-21D vector. This cloning puts the modified transposase gene under the control of the T7 promoter, rather than the natural promoter of the transposase gene. The gene product was overproduced in BL21(DE3)pLysS bacterial host cells, which do not contain the binding site for the enzyme, by specific induction in a fermentation process after cell growth is complete. (See, Studier, F. W., et al., "Use of T7 RNA Polymerase to Direct Expression of Cloned Genes," Methods Enzymol. 185:60-89 (1990)). The transposase was partially purified using the method of de la Cruz, modified by inducing overproduction at 33 or 37°C. After purification, the enzyme preparation was stored at -70°C in a storage buffer (10% glycerol, 0.7M NaCl, 20 mM Tris-HCl, pH 7.5, 0.1% Triton-X100 and 10 mM CHAPS) until use. This storage buffer is to be considered exemplary and not optimized.

A single plasmid (pRZTL1, Fig. 1) was constructed to serve as both donor and target DNA in this Example. The complete sequence of the pRZTL1 plasmid DNA is shown and described in SEQ ID NO:3. Plasmid pRZTL1 contains two Tn5 19 base pair OE termini in inverted orientation to each other. Immediately adjacent to one OE sequence is a gene that would encode tetracycline resistance, but for the lack of an upstream promoter. However, the gene is expressed if the tetracycline resistance gene is placed downstream of a transcribed region (e.g., under the control of the promoter that promotes transcription of the chloramphenicol resistance gene also present on pRZTL1). Thus, the test plasmid pRZTL1 can be assayed *in vivo* after the *in vitro* reaction to confirm that transposition has occurred. The plasmid pRZTL1 also includes an origin of replication in the transposable element, which ensures that all transposition products are plasmids that can replicate after introduction in host cells.

The following components were used in typical 20μl *in vitro* transposition reactions:

Modified transposase: 2 μl (approximately 0.1 μg enzyme/μl) in storage buffer (10% glycerol, 0.7M NaCl, 20 mM Tris-HCl, pH 7.5, 0.1% Triton-X100 and 10 mM CHAPS)

Donor/Target DNA: 18 μl (approximately 1-2 μg) in reaction buffer (at final reaction concentrations of 0.1 M potassium glutamate, 25 mM Tris acetate, pH 7.5, 10 mM Mg^{2+}-acetate, 50 μg/ml BSA, 0.5 mM β-mercaptoethanol, 2 mM spermidine, 100 μg/ml tRNA).

At 20°C, the transposase was combined with pRZTL1 DNA for about 60 minutes. Then, the reaction volume was increased by adding two volumes of reaction buffer and the temperature was raised to 37°C for 2-3 hours whereupon cleavage and strand transfer occurred.

Efficient *in vitro* transposition was shown to have occurred by *in vivo* and by *in vitro* methods. *In vivo,* many tetracycline-resistant colonies were observed after transferring the nucleic acid product of the reaction into DH5α bacterial cells. As noted, tetracycline resistance can only arise in this system if the transposable element is transposed downstream from an active promoter elsewhere on the plasmid. A typical transposition frequency was 0.1% of cells that received plasmid DNA, as determined by counting chloramphenicol resistant colonies. However, this number underestimates the total transposition event frequency because the detection system limits the target to 1/16 of the total.

Moreover, *in vitro* electrophoretic (1% agarose) and DNA sequencing analyses of DNA isolated from purified colonies revealed products of true transposition events, including both intramolecular and intermolecular events. Results of typical reactions using circular plasmid pRZTL1 substrates are shown in Lanes 4 & 5. Lane 6 of Fig. 2 shows the results obtained using linear plasmid pRZTL1 substrates.

The bands were revealed on 1% agarose gels by staining with SYBR Green (FMC BioProducts) and were scanned on a Fluorimager SI (Molecular Dynamics). In Figure 2, lane 1 shows relaxed circle, linear, and closed circle versions of pRZTL1. Lanes 2 and 3 show intramolecular and intermolecular transposition products after *in vitro* transposition of pRZTL1, respectively. The products were purified from electroporated DH5α cells and were proven by size and sequence analysis to be genuine transposition products. Lanes 4 and 5 represent products of two independent *in vitro* reactions using a mixture of closed and relaxed circular test plasmid substrates. In lane 6, linear pRZTL1 (XhoI-cut) was the reaction substrate. Lane 7 includes a BstEII digest of lambda DNA as a molecular weight standard.

Fig. 3 reproduces lanes 4, 5, and 6 of Fig. 2 and shows an analysis of various products, based upon secondary restriction digest experiments and re-electroporation and DNA sequencing. The released donor DNA corresponds to the fragment of pRZTL1 that contains the kanamycin resistance gene between the two OE sequences, or, in the case of the linear substrate, the OE-XhoI fragment. Intermolecular transposition products can be seen only as relaxed DNA circles. Intramolecular transposition products are seen as a ladder, which results from conversion of the initial superhelicity of the substrate into DNA knots. The reaction is efficient enough to achieve double transposition events that are a combination of inter- and intramolecular events.

A preliminary investigation was made into the nature of the termini involved in a transposition reaction. Wild type Tn5 OE and IE sequences were compared and an effort was undertaken to randomize the nucleotides at each of the seven positions of difference. A population of oligonucleotides degenerate at each position of difference was created. Thus, individual oligonucleotides in the population randomly included either the nucleotide of the wild type OE or the wild type IE sequence. In this scheme, 2^7 (128) distinct oligonucleotides were synthesized using conventional tools. These

oligonucleotides having sequence characteristics of both OE and IE are referred to herein as OE/IE-like sequences. To avoid nomenclature issues that arise because the oligonucleotides are intermediate between OE and IE wild type sequences, the applicants herein note that selected oligonucleotide sequences are compared to the wild type OE rather than to wild type IE, unless specifically noted. It will be appreciated by one skilled in the art that if IE is selected as the reference point, the differences are identical but are identified differently.

The following depicts the positions (x) that were varied in this mutant production scheme. WT OE is shown also at SEQ ID NO: 7, WT IE at SEQ ID NO: 10.

```
5'-CTGACTCTTATACACAAGT-3' (WT OE)
      x     xxx  x xx     (positions of difference)
5'-CTGTCTCTTGATCAGATCT-3' (WT IE)
```

In addition to the degenerate OE/IE-like sequences, the 37- base long synthetic oligonucleotides also included terminal *Sph*I and *Kpn*I restriction enzyme recognition and cleavage sites for convenient cloning of the degenerate oligonucleotides into plasmid vectors. Thus, a library of randomized termini was created from population of 2^7 (128) types of degenerate oligonucleotides.

Fig. 4 shows pRZ1496, the complete sequence of which is presented as SEQ ID NO:11. The following features are noted in the sequence:

Feature	Position
WT OE	94-112
LacZ coding	135-3137
LacY coding	3199-4486
LacA coding	4553-6295
tet^r coding	6669-9442
transposase coding	10683-12111 (Comp. Strand)
Cassette IE	12184-12225
colE1 sequence	127732-19182

The IE cassette shown in Fig. 4 was excised using *Sph*I and *Kpn*I and was replaced, using standard cleavage and ligation methods, by the synthetic termini cassettes comprising OE/IE-

like portions. Between the fixed wild type OE sequence and the OE/IE-like cloned sequence, plasmid pRZ1496 comprises a gene whose activity can be detected, namely LacZYA, as well as a selectable marker gene, tet^r. The LacZ gene is defective in that it lacks suitable transcription and translation initiation signals. The LacZ gene is transcribed and translated only when it is transposed into a position downstream from such signals.

The resulting clones were transformed using electroporation into dam^-, $LacZ^-$ bacterial cells, in this case JCM101/pOXgen cells which were grown at 37°C in LB medium under standard conditions. A dam^- strain is preferred because dam methylation can inhibit IE utilization and wild type IE sequences include two dam methylation sites. A dam^- strain eliminates dam methylation as a consideration in assessing transposition activity. The Tet^r cells selected were $LacZ^-$; transposition-activated Lac expression was readily detectable against a negative background. pOXgen is a non-essential F factor derivative that need not be provided in the host cells.

In some experiments, the EK54/MA56 transposase was encoded directly by the transformed pRZ1496 plasmid. In other experiments, the pRZ1496 plasmid was modified by deleting a unique HindIII/EagI fragment (nucleotides 9112-12083) from the plasmid (see Fig. 4) to prevent transposase production. In the latter experiments, the host cells were co-transformed with the HindIII/EagI-deleted plasmid, termed pRZ5451 (Fig. 4), and with an EK54/MA56 transposase-encoding chloramphenicol-resistant plasmid. In some experiments, a comparable plasmid encoding a wild type Tn5 transposase was used for comparison.

Transposition frequency was assessed by a papillation assay that measured the number of blue spots (Lac producing cells or "papillae") in an otherwise white colony. Transformed cells were plated (approx. 50 colonies per plate) on Glucose minimal Miller medium (Miller, J., Experiments in Molecular Genetics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1972)) containing 0.3% casamino acids, 5-bromo-4-chloro-3-indolyl-β-D-galactoside (40 μg/ml) and phenyl-β-D-galactoside (0.05%). The medium contained tetracycline (15 μg/ml) and,

where needed, chloramphenicol (20 μg/ml). Colonies that survived the selection were evaluated for transposition frequency *in vivo*. Although colonies exhibiting superior papillation were readily apparent to the naked eye, the number of blue spots per colony were determined over a period of several days (approximately 90 hours post-plating).

To show that the high-papillation phenotype was conferred by the end mutations in the plasmids, colonies were re-streaked if they appeared to have papillation levels higher than was observed when wild type IE was included on the plasmid. Colonies picked from the streaked culture plates were themselves picked and cultured. DNA was obtained and purified from the cultured cells, using standard protocols, and was transformed again into "clean" JCM101/pOXgen cells. Papillation levels were again compared with wild type IE-containing plasmids in the above-noted assays, and consistent results were observed.

To obtain DNA for sequencing of the inserted oligonucleotide, cultures were grown from white portions of 117 hyperpapillating colonies, and DNA was prepared from each colony using standard DNA miniprep methods. The DNA sequence of the OE/IE-like portion of 117 clones was determined (42 from transformations using pRZ1496 as the cloning vehicle; 75 from transformations using pRZ5451 as the cloning vehicle). Only 29 unique mutants were observed. Many mutants were isolated multiple times. All mutants that showed the highest papillation frequencies contain OE-derived bases at positions 10, 11, and 12. When the OE-like bases at these positions were maintained, it was impossible to measure the effect on transposition of other changes, since the papillation level was already extremely high.

One thousand five hundred seventy five colonies were screened as described above. The likelihood that all 128 possible mutant sequences were screened was greater than 95%. Thus, it is unlikely that other termini that contribute to a greater transformation frequency will be obtained using the tested transposase.

TABLE I.

trans papillation level of hybrid end sequences with EK54 Tnp

mutant	position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	papillation level[a]	# of times isolated[b]
IE		c	t	g	T	c	t	c	t	t	G	A	T	c	a	G	a	T	C	t	VL	0
OE					A						A	T	A			C		A	G		M	6
1											A	T	A								H	2
2											A	T	A			C					H	3
3											A	T	A					A			H	5
4											A	T	A			C		A			H	4
5											A	T	A			C			G		H	6
6											A	T	A					A	G		H	6
7											A	T	A			C		A	G		H	4
8											A	T	A						G		M	7
9					A						A	T	A								M	3
10					A						A	T	A			C					M	2
11					A						A	T	A					A			M	1
12					A						A	T	A						G			0
13					A						A	T	A			C		A				0
14					A						A	T	A			C			G		M	4
15					A						A	T						A	G		M	4
16											A	T				C		A			L	2
17											A	T						A	G		L	1
18											A	T				C		A	G		L	2
19											A					C		A	G		L	1
20												T				C		A	G		L	1
21																C		A	G		L	1

All hybrid end sequences isolated on pRZ5451 that papillate more frequently than wt IE, when the EK54 Tnp is expressed from pFMA187, are listed. [a]*trans* papillation levels of wt IE, wt OE and hybrid end sequences are classified as follows: VL-very low, L-low, M-medium, and H-high. [b]Although mutants 12 and 13 were not found in this experiment, they were found in *cis* papillation screening (Table II).

TABLE II.
cis papillation level of hybrid end sequences with EK54 Tnp

mutant	position 1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	papillation level[a]	# of times isolated[b]
IE	c	t	g	T	c	t	c	t	t	G	A	T	c	a	G	a	T	C	t	L	0
OE				A						A	T	A			C		A	G		H	2
1										A	T	A								H	2
2										A	T	A			C						0
3										A	T	A					A			H	1
4										A	T	A			C		A			H	1
5										A	T	A			C			G		H	1
6										A	T	A					A	G		H	2
7										A	T	A			C		A	G		H	3
8										A	T	A						G		H	1
9				A						A	T	A								H	1
10				A						A	T	A			C						0
11				A						A	T	A					A			H	2
12				A						A	T	A						G		MH	3
13				A						A	T	A			C		A			MH	1
14				A						A	T	A			C			G			0
15				A						A	T	A					A	G		H	2
16										A	T				C					M	1
17										A	T						A	G		M	1
18				A						A	T				C					M	2
19				A						A	T				C		A			M	2
20				A						A	T				C		A	G		M	1
21										A		A					A			M	4
22										A		A						G		M	1
23										A		A			C		A	G		M	1
24										A					C		A			M	1
25										A					C		A	G		M	1
26											T				C		A	G		M	1
27															C		A	G		M	2

All hybrid end sequences isolated on pRZ1496 that papillate more frequently than wt IE, when the EK54 Tnp is expressed from the same plasmid, are listed. [a]*cis* papillation levels of wt IE, wt OE and hybrid end sequences are classified as follows: L-low, M-medium, MH-medium high, and H-high. [b]Although mutants 2, 10 and 14 were not found in this experiment, they were found in *trans* papillation screening (Table I).

Tables I and II report the qualitative papillation level of mutant constructs carrying the indicated hybrid end sequences or the wild type OE or IE end sequences. In the tables, the sequence at each position of the terminus corresponds to wild type IE unless otherwise noted. The applicants intend that, while the sequences are presented in shorthand notation, one of ordinary skill can readily determine the complete 19 base pair sequence of every presented mutant, and this specification is to be read to include all such complete sequences. Table I includes data from trials where the EK54 transposase was provided *in trans*; Table II, from those trials where the EK54 transposase was provided *in cis*. Although a transposase provided *in cis* is more active in absolute terms than a transposase provided *in trans*, the *cis* or *trans* source of the transposase does not alter the relative *in vivo* transposition frequencies of the tested termini.

Tables I and II show that every mutant that retains ATA at positions 10, 11, and 12, respectively, had an activity comparable to, or higher than, wild type OE, regardless of whether the wild type OE activity was medium (Table I, *trans*) or high (Table II, *cis*). Moreover, whenever that three-base sequence in a mutant was not ATA, the mutant exhibited lower papillation activity than wild type OE. It was also noted that papillation is at least comparable to, and tends to be significantly higher than, wild type OE when position 4 is a T.

Quantitative analysis of papillation levels was difficult, beyond the comparative levels shown (very low, low, medium, medium high, and high). However, one skilled in the art can readily note the papillation level of OE and can recognize those colonies having comparable or higher levels. It is helpful to observe the papillae with magnification.

The number of observed papillae increased over time, as is shown in Figs 5 - 7 which roughly quantitate the papillation observed in cells transformed separately with 9 clones containing either distinct synthetic termini cassettes or wild type OE or IE termini. In these 3 figures, each mutant is identified by its differences from the wild type IE sequence.

Note that, among the tested mutants, only mutant 10A/11T/12A had a higher transposition papillation level than wild type OE. That mutant, which would be called mutant 4/15/17/18 when OE is the reference sequence) was the only mutant of those shown in Figs. 5-7 that retained the nucleotides ATA at positions 10, 11, and 12. Figs. 5 (y-axis: 0 - 1500 papillae) and 6 (y-axis: 0 - 250 papillae) show papillation using various mutants plus IE and OE controls and the EK54/MA56 enzyme. Fig. 7 (y-axis: 0 - 250 papillae), shows papillation when the same mutant sequences were tested against the wild type (more properly, MA56) transposase. The 10A/11T/12A mutant (SEQ ID NO: 9) yielded significantly more papillae (approximately 3000) in a shorter time (68 hours) with ED54/MA56 transposase than was observed even after 90 hours with the WT OE (approximately 1500). A single OE-like nucleotide at position 15 on an IE-like background also increased papillation frequency.

In vivo transposition frequency was also quantitated in a tetracycline-resistance assay using two sequences having high levels of hyperpapillation. These sequences were 5'-CTGTCTCTTATACACATCT-3' (SEQ ID NO: 8), which differs from the wild type OE sequence at positions 4, 17, and 18, counting from the 5' end, and 5'-CTGTCTCTTATACAGATCT-3' (SEQ ID NO: 9), which differs from the wild type OE at positions 4, 15, 17, and 18. These sequences are considered the preferred mutant termini in an assay using a transposase that contains EK54/MA56 or a transposase that contains MA56. Each sequence was separately engineered into pRZTL1 in place of the plasmid's two wild type OE sequences. A PCR-amplified fragment containing the desired ends flanking the kanamycin resistance gene was readily cloned into the large HindIII fragment of pRZTL1. The resulting plasmids are identical to pRZTL1 except at the indicated termini. For comparison, pRZTL1 and a derivative of pRZTL1 containing two wild type IE sequences were also tested. In the assay, JCM101/pOXgen cells were co-transformed with a test plasmid (pRZTL1 or derivative) and a high copy number amp^r plasmid that encoded either the EK54/MA56 transposase or wild type (MA56) transposase. The host cells become tetracycline

resistant only when a transposition event brings the Tet^r gene into downstream proximity with a suitable transcriptional promoter elsewhere on a plasmid or on the chromosome. The total number of cells that received the test plasmids was determined by counting chloramphenicol resistant, ampicillin resistant colonies. Transposition frequency was calculated by taking the ratio of $tet^r/cam^r amp^r$ colonies. Approximately 40 to 60 fold increase over wild type OE in *in vivo* transposition was observed when using either of the mutant termini and EK54/MA56 transposase. Of the two preferred mutant termini, the one containing mutations at three positions relative to the wild type OE sequence yielded a higher increase.

As is shown in Fig. 8, which plots the tested plasmid against the transposition frequency ($\times 10^{-8}$), little transposition was seen when the test plasmid included two IE termini. Somewhat higher transposition was observed when the test plasmid included two OE termini, particularly when the EK54/MA56 transposase was employed. In striking contrast, the combination of the EK54/MA56 transposase with either of the preferred selected ends (containing OE-like bases only at positions 10, 11, and 12, or positions 10, 11, 12, and 15) yielded a great increase in *in vivo* transposition over wild type OE termini.

The preferred hyperactive mutant terminus having the most preferred synthetic terminus sequence 5'-CTGTCTCTTATACACATCT-3' (SEQ ID NO: 8) was provided in place of both WT OE termini in pRZTL1 (Fig. 4) and was tested in the *in vitro* transposition assay of the present invention using the triple mutant transposase described herein. This mutant terminus was chosen for further *in vitro* analysis because its transposition frequency was higher than for the second preferred synthetic terminus and because it has no dam methylation sites, so dam methylation no longer affects transposition frequency. In contrast the 4/15/17/18 mutant does have a dam methylation site.

In a preliminary experiment, CHAPS was eliminated from the reaction, but the pre-incubation step was used. The reaction

was pre-incubated for 1 hour at 20°C, then diluted two times, and then incubated for 3 hours at 37°C. About 0.5 μg of DNA and 0.4μg of transposase was used. The transposition products were observed on a gel. With the mutant termini, very little of the initial DNA was observed. Numerous bands representing primary and secondary transposition reaction products were observed. The reaction mixtures were transformed into DH5α cells and were plated on chloramphenicol-, tetracycline-, or kanamycin-containing plates.

Six hundred forty chloramphenicol-resistant colonies were observed. Although these could represent unreacted plasmid, all such colonies tested (n=12) were sensitive to kanamycin, which indicates a loss of donor backbone DNA. All twelve colonies also included plasmids of varied size; 9 of the 12 were characterized as deletion-inversions, the remaining 3 were simple deletions. Seventy nine tetracycline-resistant colonies were observed, which indicated an activation of the tet^r gene by transposition.

Eleven kanamycin resistant colonies were observed. This indicated a low percentage of remaining plasmids carrying the donor backbone DNA.

In a second, similar test, about 1 μg of plasmid DNA and 0.2 μg transposase were used. In this test, the reaction was incubated without CHAPS at 37°C for 3 hours without pre-incubation or dilution. Some initial DNA was observed in the gel after the 3 hour reaction. After overnight incubation, only transposition products were observed.

The 3 hour reaction products were transformed into DH5α cells and plated as described. About 50% of the chloramphenicol resistant colonies were sensitive to kanamycin and were presumably transposition products.

The invention is not intended to be limited to the foregoing examples, but to encompass all such modifications and variations as come within the scope of the appended claims. It is envisioned that, in addition to the uses specifically noted herein, other applications will be apparent to the skilled molecular biologist. In particular, methods for

introducing desired mutations into prokaryotic or eukaryotic DNA are very desirable. For example, at present it is difficult to knock out a functional eukaryotic gene by homologous recombination with an inactive version of the gene that resides on a plasmid. The difficulty arises from the need to flank the gene on the plasmid with extensive upstream and downstream sequences. Using this system, however, an inactivating transposable element containing a selectable marker gene (e.g., neo) can be introduced *in vitro* into a plasmid that contains the gene that one desires to inactivate. After transposition, the products can be introduced into suitable host cells. Using standard selection means, one can recover only cell colonies that contain a plasmid having the transposable element. Such plasmids can be screened, for example by restriction analysis, to recover those that contain a disrupted gene. Such clones can then be introduced directly into eukaryotic cells for homologous recombination and selection using the same marker gene.

Also, one can use the system to readily insert a PCR-amplified DNA fragment into a vector, thus avoiding traditional cloning steps entirely. This can be accomplished by (1) providing suitable a pair of PCR primers containing OE termini adjacent to the sequence-specific parts of the primers, (2) performing standard PCR amplification of a desired nucleic acid fragment, (3) performing the *in vitro* transposition reaction of the present invention using the double-stranded products of PCR amplification as the donor DNA.

SEQUENCE LISTING

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(F) ZIP: 53703

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Berson, Bennett J
(B) REGISTRATION NUMBER: 37094
(C) REFERENCE/DOCKET NUMBER: 960296.94142

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 608/251-5000
(B) TELEFAX: 608-251-9166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Gene encoding modified Tn5 transposase enzyme"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 93..1523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGACTCTTA TACACAAGTA GCGTCCTGAA CGGAACCTTT CCCGTTTTCC AGGATCTGAT 60

CTTCCATGTG ACCTCCTAAC ATGGTAACGT TC ATG ATA ACT TCT GCT CTT CAT 113
Met Ile Thr Ser Ala Leu His
1 5

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CGT GCG GCC GAC TGG GCT AAA TCT GTG TTC TCT TCG GCG GCG CTG GGT      161
Arg Ala Ala Asp Trp Ala Lys Ser Val Phe Ser Ser Ala Ala Leu Gly
         10                  15                  20

GAT CCT CGC CGT ACT GCC CGC TTG GTT AAC GTC GCC GCC CAA TTG GCA      209
Asp Pro Arg Arg Thr Ala Arg Leu Val Asn Val Ala Ala Gln Leu Ala
     25                  30                  35

AAA TAT TCT GGT AAA TCA ATA ACC ATC TCA TCA GAG GGT AGT AAA GCC      257
Lys Tyr Ser Gly Lys Ser Ile Thr Ile Ser Ser Glu Gly Ser Lys Ala
 40                  45                  50                  55

GCC CAG GAA GGC GCT TAC CGA TTT ATC CGC AAT CCC AAC GTT TCT GCC      305
Ala Gln Glu Gly Ala Tyr Arg Phe Ile Arg Asn Pro Asn Val Ser Ala
                 60                  65                  70

GAG GCG ATC AGA AAG GCT GGC GCC ATG CAA ACA GTC AAG TTG GCT CAG      353
Glu Ala Ile Arg Lys Ala Gly Ala Met Gln Thr Val Lys Leu Ala Gln
             75                  80                  85

GAG TTT CCC GAA CTG CTG GCC ATT GAG GAC ACC ACC TCT TTG AGT TAT      401
Glu Phe Pro Glu Leu Leu Ala Ile Glu Asp Thr Thr Ser Leu Ser Tyr
         90                  95                 100

CGC CAC CAG GTC GCC GAA GAG CTT GGC AAG CTG GGC TCT ATT CAG GAT      449
Arg His Gln Val Ala Glu Glu Leu Gly Lys Leu Gly Ser Ile Gln Asp
     105                 110                 115

AAA TCC CGC GGA TGG TGG GTT CAC TCC GTT CTC TTG CTC GAG GCC ACC      497
Lys Ser Arg Gly Trp Trp Val His Ser Val Leu Leu Leu Glu Ala Thr
 120                 125                 130                 135

ACA TTC CGC ACC GTA GGA TTA CTG CAT CAG GAG TGG TGG ATG CGC CCG      545
Thr Phe Arg Thr Val Gly Leu Leu His Gln Glu Trp Trp Met Arg Pro
                 140                 145                 150

GAT GAC CCT GCC GAT GCG GAT GAA AAG GAG AGT GGC AAA TGG CTG GCA      593
Asp Asp Pro Ala Asp Ala Asp Glu Lys Glu Ser Gly Lys Trp Leu Ala
             155                 160                 165

GCG GCC GCA ACT AGC CGG TTA CGC ATG GGC AGC ATG ATG AGC AAC GTG      641
Ala Ala Ala Thr Ser Arg Leu Arg Met Gly Ser Met Met Ser Asn Val
         170                 175                 180

ATT GCG GTC TGT GAC CGC GAA GCC GAT ATT CAT GCT TAT CTG CAG GAC      689
Ile Ala Val Cys Asp Arg Glu Ala Asp Ile His Ala Tyr Leu Gln Asp
     185                 190                 195

AGG CTG GCG CAT AAC GAG CGC TTC GTG GTG CGC TCC AAG CAC CCA CGC      737
Arg Leu Ala His Asn Glu Arg Phe Val Val Arg Ser Lys His Pro Arg
 200                 205                 210                 215

AAG GAC GTA GAG TCT GGG TTG TAT CTG ATC GAC CAT CTG AAG AAC CAA      785
Lys Asp Val Glu Ser Gly Leu Tyr Leu Ile Asp His Leu Lys Asn Gln
                 220                 225                 230

CCG GAG TTG GGT GGC TAT CAG ATC AGC ATT CCG CAA AAG GGC GTG GTG      833
Pro Glu Leu Gly Gly Tyr Gln Ile Ser Ile Pro Gln Lys Gly Val Val
             235                 240                 245

GAT AAA CGC GGT AAA CGT AAA AAT CGA CCA GCC CGC AAG GCG AGC TTG      881
Asp Lys Arg Gly Lys Arg Lys Asn Arg Pro Ala Arg Lys Ala Ser Leu
         250                 255                 260

AGC CTG CGC AGT GGG CGC ATC ACG CTA AAA CAG GGG AAT ATC ACG CTC      929
Ser Leu Arg Ser Gly Arg Ile Thr Leu Lys Gln Gly Asn Ile Thr Leu
     265                 270                 275
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AAC GCG GTG CTG GCC GAG GAG ATT AAC CCG CCC AAG GGT GAG ACC CCG        977
Asn Ala Val Leu Ala Glu Glu Ile Asn Pro Pro Lys Gly Glu Thr Pro
280                 285                 290                 295

TTG AAA TGG TTG TTG CTG ACC GGC GAA CCG GTC GAG TCG CTA GCC CAA       1025
Leu Lys Trp Leu Leu Leu Thr Gly Glu Pro Val Glu Ser Leu Ala Gln
                300                 305                 310

GCC TTG CGC GTC ATC GAC ATT TAT ACC CAT CGC TGG CGG ATC GAG GAG       1073
Ala Leu Arg Val Ile Asp Ile Tyr Thr His Arg Trp Arg Ile Glu Glu
            315                 320                 325

TTC CAT AAG GCA TGG AAA ACC GGA GCA GGA GCC GAG AGG CAA CGC ATG       1121
Phe His Lys Ala Trp Lys Thr Gly Ala Gly Ala Glu Arg Gln Arg Met
        330                 335                 340

GAG GAG CCG GAT AAT CTG GAG CGG ATG GTC TCG ATC CTC TCG TTT GTT       1169
Glu Glu Pro Asp Asn Leu Glu Arg Met Val Ser Ile Leu Ser Phe Val
    345                 350                 355

GCG GTC AGG CTG TTA CAG CTC AGA GAA AGC TTC ACG CCG CCG CAA GCA       1217
Ala Val Arg Leu Leu Gln Leu Arg Glu Ser Phe Thr Pro Pro Gln Ala
360                 365                 370                 375

CTC AGG GCG CAA GGG CTG CTA AAG GAA GCG GAA CAC GTA GAA AGC CAG       1265
Leu Arg Ala Gln Gly Leu Leu Lys Glu Ala Glu His Val Glu Ser Gln
                380                 385                 390

TCC GCA GAA ACG GTG CTG ACC CCG GAT GAA TGT CAG CTA CTG GGC TAT       1313
Ser Ala Glu Thr Val Leu Thr Pro Asp Glu Cys Gln Leu Leu Gly Tyr
            395                 400                 405

CTG GAC AAG GGA AAA CGC AAG CGC AAA GAG AAA GCA GGT AGC TTG CAG       1361
Leu Asp Lys Gly Lys Arg Lys Arg Lys Glu Lys Ala Gly Ser Leu Gln
        410                 415                 420

TGG GCT TAC ATG GCG ATA GCT AGA CTG GGC GGT TTT ATG GAC AGC AAG       1409
Trp Ala Tyr Met Ala Ile Ala Arg Leu Gly Gly Phe Met Asp Ser Lys
    425                 430                 435

CGA ACC GGA ATT GCC AGC TGG GGC GCC CTC TGG GAA GGT TGG GAA GCC       1457
Arg Thr Gly Ile Ala Ser Trp Gly Ala Leu Trp Glu Gly Trp Glu Ala
440                 445                 450                 455

CTG CAA AGT AAA CTG GAT GGC TTT CTT GCC GCC AAG GAT CTG ATG GCG       1505
Leu Gln Ser Lys Leu Asp Gly Phe Leu Ala Ala Lys Asp Leu Met Ala
                460                 465                 470

CAG GGG ATC AAG ATC TGA TCAAGAGACA G                                 1534
Gln Gly Ile Lys Ile  *
            475
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ile Thr Ser Ala Leu His Arg Ala Ala Asp Trp Ala Lys Ser Val
  1               5                  10                  15
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Phe Ser Ser Ala Ala Leu Gly Asp Pro Arg Arg Thr Ala Arg Leu Val
20 25 30

Asn Val Ala Ala Gln Leu Ala Lys Tyr Ser Gly Lys Ser Ile Thr Ile
35 40 45

Ser Ser Glu Gly Ser Lys Ala Ala Gln Glu Gly Ala Tyr Arg Phe Ile
50 55 60

Arg Asn Pro Asn Val Ser Ala Glu Ala Ile Arg Lys Ala Gly Ala Met
65 70 75 80

Gln Thr Val Lys Leu Ala Gln Glu Phe Pro Glu Leu Leu Ala Ile Glu
85 90 95

Asp Thr Thr Ser Leu Ser Tyr Arg His Gln Val Ala Glu Glu Leu Gly
100 105 110

Lys Leu Gly Ser Ile Gln Asp Lys Ser Arg Gly Trp Trp Val His Ser
115 120 125

Val Leu Leu Leu Glu Ala Thr Thr Phe Arg Thr Val Gly Leu Leu His
130 135 140

Gln Glu Trp Trp Met Arg Pro Asp Asp Pro Ala Asp Ala Asp Glu Lys
145 150 155 160

Glu Ser Gly Lys Trp Leu Ala Ala Ala Thr Ser Arg Leu Arg Met
165 170 175

Gly Ser Met Met Ser Asn Val Ile Ala Val Cys Asp Arg Glu Ala Asp
180 185 190

Ile His Ala Tyr Leu Gln Asp Arg Leu Ala His Asn Glu Arg Phe Val
195 200 205

Val Arg Ser Lys His Pro Arg Lys Asp Val Glu Ser Gly Leu Tyr Leu
210 215 220

Ile Asp His Leu Lys Asn Gln Pro Glu Leu Gly Gly Tyr Gln Ile Ser
225 230 235 240

Ile Pro Gln Lys Gly Val Val Asp Lys Arg Gly Lys Arg Lys Asn Arg
245 250 255

Pro Ala Arg Lys Ala Ser Leu Ser Leu Arg Ser Gly Arg Ile Thr Leu
260 265 270

Lys Gln Gly Asn Ile Thr Leu Asn Ala Val Leu Ala Glu Glu Ile Asn
275 280 285

Pro Pro Lys Gly Glu Thr Pro Leu Lys Trp Leu Leu Leu Thr Gly Glu
290 295 300

Pro Val Glu Ser Leu Ala Gln Ala Leu Arg Val Ile Asp Ile Tyr Thr
305 310 315 320

His Arg Trp Arg Ile Glu Glu Phe His Lys Ala Trp Lys Thr Gly Ala
325 330 335

Gly Ala Glu Arg Gln Arg Met Glu Glu Pro Asp Asn Leu Glu Arg Met
340 345 350

Val Ser Ile Leu Ser Phe Val Ala Val Arg Leu Leu Gln Leu Arg Glu
355 360 365

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Ser Phe Thr Pro Pro Gln Ala Leu Arg Ala Gln Gly Leu Leu Lys Glu
370                 375                 380

Ala Glu His Val Glu Ser Gln Ser Ala Glu Thr Val Leu Thr Pro Asp
385                 390                 395                 400

Glu Cys Gln Leu Leu Gly Tyr Leu Asp Lys Gly Lys Arg Lys Arg Lys
                405                 410                 415

Glu Lys Ala Gly Ser Leu Gln Trp Ala Tyr Met Ala Ile Ala Arg Leu
            420                 425                 430

Gly Gly Phe Met Asp Ser Lys Arg Thr Gly Ile Ala Ser Trp Gly Ala
        435                 440                 445

Leu Trp Glu Gly Trp Glu Ala Leu Gln Ser Lys Leu Asp Gly Phe Leu
450                 455                 460

Ala Ala Lys Asp Leu Met Ala Gln Gly Ile Lys Ile  *
465                 470                 475
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5838 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Plasmid DNA"

(vii) IMMEDIATE SOURCE:
(B) CLONE: pRZTL1

(ix) FEATURE:
(A) NAME/KEY: insertion_seq
(B) LOCATION: 1..19

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 77..1267
(D) OTHER INFORMATION: /function= "tetracycline resistance"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: complement (2301..2960)
(D) OTHER INFORMATION: /function= "chloramphenicol resistance"

(ix) FEATURE:
(A) NAME/KEY: insertion_seq
(B) LOCATION: 4564..4582

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 4715..5530
(D) OTHER INFORMATION: /function= "kanamycin resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CTGACTCTTA TACACAAGTA AGCTTTAATG CGGTAGTTTA TCACAGTTAA ATTGCTAACG      60

CAGTCAGGCA CCGTGT ATG AAA TCT AAC AAT GCG CTC ATC GTC ATC CTC         109
                  Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu
                      480                 485
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GGC ACC GTC ACC CTG GAT GCT GTA GGC ATA GGC TTG GTT ATG CCG GTA        157
Gly Thr Val Thr Leu Asp Ala Val Gly Ile Gly Leu Val Met Pro Val
    490                 495                 500

CTG CCG GGC CTC TTG CGG GAT ATC GTC CAT TCC GAC AGC ATC GCC AGT        205
Leu Pro Gly Leu Leu Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser
505                 510                 515                 520

CAC TAT GGC GTG CTG CTA GCG CTA TAT GCG TTG ATG CAA TTT CTA TGC        253
His Tyr Gly Val Leu Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys
                525                 530                 535

GCA CCC GTT CTC GGA GCA CTG TCC GAC CGC TTT GGC CGC CGC CCA GTC        301
Ala Pro Val Leu Gly Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val
            540                 545                 550

CTG CTC GCT TCG CTA CTT GGA GCC ACT ATC GAC TAC GCG ATC ATG GCG        349
Leu Leu Ala Ser Leu Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala
        555                 560                 565

ACC ACA CCC GTC CTG TGG ATC CTC TAC GCC GGA CGC ATC GTG GCC GGC        397
Thr Thr Pro Val Leu Trp Ile Leu Tyr Ala Gly Arg Ile Val Ala Gly
    570                 575                 580

ATC ACC GGC GCC ACA GGT GCG GTT GCT GGC GCC TAT ATC GCC GAC ATC        445
Ile Thr Gly Ala Thr Gly Ala Val Ala Gly Ala Tyr Ile Ala Asp Ile
585                 590                 595                 600

ACC GAT GGG GAA GAT CGG GCT CGC CAC TTC GGG CTC ATG AGC GCT TGT        493
Thr Asp Gly Glu Asp Arg Ala Arg His Phe Gly Leu Met Ser Ala Cys
                605                 610                 615

TTC GGC GTG GGT ATG GTG GCA GGC CCC GTG GCC GGG GGA CTG TTG GGC        541
Phe Gly Val Gly Met Val Ala Gly Pro Val Ala Gly Gly Leu Leu Gly
            620                 625                 630

GCC ATC TCC TTG CAT GCA CCA TTC CTT GCG GCG GCG GTG CTC AAC GGC        589
Ala Ile Ser Leu His Ala Pro Phe Leu Ala Ala Ala Val Leu Asn Gly
        635                 640                 645

CTC AAC CTA CTA CTG GGC TGC TTC CTA ATG CAG GAG TCG CAT AAG GGA        637
Leu Asn Leu Leu Leu Gly Cys Phe Leu Met Gln Glu Ser His Lys Gly
    650                 655                 660

GAG CGT CGA CCG ATG CCC TTG AGA GCC TTC AAC CCA GTC AGC TCC TTC        685
Glu Arg Arg Pro Met Pro Leu Arg Ala Phe Asn Pro Val Ser Ser Phe
665                 670                 675                 680

CGG TGG GCG CGG GGC ATG ACT ATC GTC GCC GCA CTT ATG ACT GTC TTC        733
Arg Trp Ala Arg Gly Met Thr Ile Val Ala Ala Leu Met Thr Val Phe
                685                 690                 695

TTT ATC ATG CAA CTC GTA GGA CAG GTG CCG GCA GCG CTC TGG GTC ATT        781
Phe Ile Met Gln Leu Val Gly Gln Val Pro Ala Ala Leu Trp Val Ile
            700                 705                 710

TTC GGC GAG GAC CGC TTT CGC TGG AGC GCG ACG ATG ATC GGC CTG TCG        829
Phe Gly Glu Asp Arg Phe Arg Trp Ser Ala Thr Met Ile Gly Leu Ser
        715                 720                 725

CTT GCG GTA TTC GGA ATC TTG CAC GCC CTC GCT CAA GCC TTC GTC ACT        877
Leu Ala Val Phe Gly Ile Leu His Ala Leu Ala Gln Ala Phe Val Thr
    730                 735                 740

GGT CCC GCC ACC AAA CGT TTC GGC GAG AAG CAG GCC ATT ATC GCC GGC        925
Gly Pro Ala Thr Lys Arg Phe Gly Glu Lys Gln Ala Ile Ile Ala Gly
745                 750                 755                 760
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ATG GCG GCC GAC GCG CTG GGC TAC GTC TTG CTG GCG TTC GCG ACG CGA      973
Met Ala Ala Asp Ala Leu Gly Tyr Val Leu Leu Ala Phe Ala Thr Arg
                765                 770                 775

GGC TGG ATG GCC TTC CCC ATT ATG ATT CTT CTC GCT TCC GGC GGC ATC     1021
Gly Trp Met Ala Phe Pro Ile Met Ile Leu Leu Ala Ser Gly Gly Ile
            780                 785                 790

GGG ATG CCC GCG TTG CAG GCC ATG CTG TCC AGG CAG GTA GAT GAC GAC     1069
Gly Met Pro Ala Leu Gln Ala Met Leu Ser Arg Gln Val Asp Asp Asp
        795                 800                 805

CAT CAG GGA CAG CTT CAA GGA TCG CTC GCG GCT CTT ACC AGC CTA ACT     1117
His Gln Gly Gln Leu Gln Gly Ser Leu Ala Ala Leu Thr Ser Leu Thr
    810                 815                 820

TCG ATC ACT GGA CCG CTG ATC GTC ACG GCG ATT TAT GCC GCC TCG GCG     1165
Ser Ile Thr Gly Pro Leu Ile Val Thr Ala Ile Tyr Ala Ala Ser Ala
825                 830                 835                 840

AGC ACA TGG AAC GGG TTG GCA TGG ATT GTA GGC GCC GCC CTA TAC CTT     1213
Ser Thr Trp Asn Gly Leu Ala Trp Ile Val Gly Ala Ala Leu Tyr Leu
                845                 850                 855

GTC TGC CTC CCC GCG TTG CGT CGC GGT GCA TGG AGC CGG GCC ACC TCG     1261
Val Cys Leu Pro Ala Leu Arg Arg Gly Ala Trp Ser Arg Ala Thr Ser
            860                 865                 870

ACC TGA ATGGAAGCCG GCGGCACCTC GCTAACGGAT TCACCACTCC AAGAATTGGA      1317
Thr  *

GCCAATCAAT TCTTGCGGAG AACTGTGAAT GCGCAAACCA ACCCTTGGCA GAACATATCC  1377

ATCGCGTCCG CCATCTCCAG CAGCCGCACG CGGCGCATCT CGGGCAGCGT TGGGTCCTGG  1437

CCACGGGTGC GCATGATCGT GCTCCTGTCG TTGAGGACCC GGCTAGGCTG GCGGGGTTGC  1497

CTTACTGGTT AGCAGAATGA ATCACCGATA CGCGAGCGAA CGTGAAGCGA CTGCTGCTGC  1557

AAAACGTCTG CGACCTGAGC AACAACATGA ATGGTCTTCG GTTTCCGTGT TTCGTAAAGT  1617

CTGGAAACGC GGAAGTCCCC TACGTGCTGC TGAAGTTGCC CGCAACAGAG AGTGGAACCA  1677

ACCGGTGATA CCACGATACT ATGACTGAGA GTCAACGCCA TGAGCGGCCT CATTTCTTAT  1737

TCTGAGTTAC AACAGTCCGC ACCGCTGTCC GGTAGCTCCT TCCGGTGGGC GCGGGGCATG  1797

ACTATCGTCG CCGCACTTAT GACTGTCTTC TTTATCATGC AACTCGTAGG ACAGGTGCCG  1857

GCAGCGCCCA ACAGTCCCCC GGCCACGGGG CCTGCCACCA TACCCACGCC GAAACAAGCG  1917

CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC CTGTGGAACA  1977

CCTACATCTG TATTAACGAA GCGCTAACCG TTTTTATCAG GCTCTGGGAG GCAGAATAAA  2037

TGATCATATC GTCAATTATT ACCTCCACGG GGAGAGCCTG AGCAAACTGG CCTCAGGCAT  2097

TTGAGAAGCA CACGGTCACA CTGCTTCCGG TAGTCAATAA ACCGGTAAAC CAGCAATAGA  2157

CATAAGCGGC TATTTAACGA CCCTGCCCTG AACCGACGAC CGGGTCGAAT TTGCTTTCGA  2217

ATTTCTGCCA TTCATCCGCT TATTATCAAT TATTCAGGCG TAGCACCAGG CGTTTAAGGG  2277

CACCAATAAC TGCCTTAAAA AAATTACGCC CCGCCCTGCC ACTCATCGCA GTACTGTTGT  2337

AATTCATTAA GCATTCTGCC GACATGGAAG CCATCACAGA CGGCATGATG AACCTGAATC  2397
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GCCAGCGGCA TCAGCACCTT GTCGCCTTGC GTATAATATT TGCCCATGGT GAAAACGGGG 2457
GCGAAGAAGT TGTCCATATT GGCCACGTTT AAATCAAAAC TGGTGAAACT CACCCAGGGA 2517
TTGGCTGAGA CGAAAAACAT ATTCTCAATA AACCCTTTAG GGAAATAGGC CAGGTTTTCA 2577
CCGTAACACG CCACATCTTG CGAATATATG TGTAGAAACT GCCGGAAATC GTCGTGGTAT 2637
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ACACTATCCC ATATCACCAG CTCACCGTCT TTCATTGCCA TACGGAATTC CGGATGAGCA 2757
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CGATCAACGT CTCATTTTCG CCAAAAGTTG GCCCAGGGCT TCCCGGTATC AACAGGGACA 3117
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GTCAGCAGAA TATGTGATAC AGGATATATT CCGCTTCCTC GCTCACTGAC TCGCTACGCT 3477
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CCTGCCTTTC GGTTTACCGG TGTCATTCCG CTGTTATGGC CGCGTTTGTC TCATTCCACG 3777
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GCCAGTTACC TCGGTTCAAA GAGTTGGTAG CTCAGAGAAC CTTCGAAAAA CCGCCCTGCA 4077
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ATCATCTTAT TAATCAGATA AAATATTTCT AGAGGTGAAC CATCACCCTA ATCAAGTTTT 4197
TTGGGGTCGA GGTGCCGTAA AGCACTAAAT CGGAACCCTA AAGGGATGCC CCGATTTAGA 4257
GCTTGACGGG GAAAGCCGGC GAACGTGGCG AGAAAGGAAG GGAAGAAAGC GAAAGGAGCG 4317
GGCGCTAGGG CGCTGGCAAG TGTAGCGGTC ACGCTGCGCG TAACCACCAC ACCCGCCGCG 4377
CTTAATGCGC CGCTACAGCG CCATTCGCCA TTCAGGCTGC GCAACTGTTG GGAAGGGCGA 4437

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TCGGTGCGGG CCTCTTCGCT ATTACGCCAG CTGGCGAAAG GGGGATGTGC TGCAAGGCGA    4497

TTAAGTTGGG TAACGCCAGG GTTTTCCCAG TCACGACGTT GTAAAACGAC GGCCAGTGCC    4557

AAGCTTACTT GTGTATAAGA GTCAGTCGAC CTGCAGGGGG GGGGGGGAAA GCCACGTTGT    4617

GTCTCAAAAT CTCTGATGTT ACATTGCACA AGATAAAAAT ATATCATCAT GAACAATAAA    4677

ACTGTCTGCT TACATAAACA GTAATACAAG GGGTGTT ATG AGC CAT ATT CAA CGG      4732
                                          Met Ser His Ile Gln Arg
                                            1               5

GAA ACG TCT TGC TCG AGG CCG CGA TTA AAT TCC AAC ATG GAT GCT GAT      4780
Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn Ser Asn Met Asp Ala Asp
            10                  15                  20

TTA TAT GGG TAT AAA TGG GCT CGC GAT AAT GTC GGG CAA TCA GGT GCG      4828
Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn Val Gly Gln Ser Gly Ala
        25                  30                  35

ACA ATC TAT CGA TTG TAT GGG AAG CCC GAT GCG CCA GAG TTG TTT CTG      4876
Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp Ala Pro Glu Leu Phe Leu
    40                  45                  50

AAA CAT GGC AAA GGT AGC GTT GCC AAT GAT GTT ACA GAT GAG ATG GTC      4924
Lys His Gly Lys Gly Ser Val Ala Asn Asp Val Thr Asp Glu Met Val
55                  60                  65                  70

AGA CTA AAC TGG CTG ACG GAA TTT ATG CCT CTT CCG ACC ATC AAG CAT      4972
Arg Leu Asn Trp Leu Thr Glu Phe Met Pro Leu Pro Thr Ile Lys His
                75                  80                  85

TTT ATC CGT ACT CCT GAT GAT GCA TGG TTA CTC ACC ACT GCG ATC CCC      5020
Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu Leu Thr Thr Ala Ile Pro
            90                  95                  100

GGG AAA ACA GCA TTC CAG GTA TTA GAA GAA TAT CCT GAT TCA GGT GAA      5068
Gly Lys Thr Ala Phe Gln Val Leu Glu Glu Tyr Pro Asp Ser Gly Glu
        105                 110                 115

AAT ATT GTT GAT GCG CTG GCA GTG TTC CTG CGC CGG TTG CAT TCG ATT      5116
Asn Ile Val Asp Ala Leu Ala Val Phe Leu Arg Arg Leu His Ser Ile
    120                 125                 130

CCT GTT TGT AAT TGT CCT TTT AAC AGC GAT CGC GTA TTT CGT CTC GCT      5164
Pro Val Cys Asn Cys Pro Phe Asn Ser Asp Arg Val Phe Arg Leu Ala
135                 140                 145                 150

CAG GCG CAA TCA CGA ATG AAT AAC GGT TTG GTT GAT GCG AGT GAT TTT      5212
Gln Ala Gln Ser Arg Met Asn Asn Gly Leu Val Asp Ala Ser Asp Phe
                155                 160                 165

GAT GAC GAG CGT AAT GGC TGG CCT GTT GAA CAA GTC TGG AAA GAA ATG      5260
Asp Asp Glu Arg Asn Gly Trp Pro Val Glu Gln Val Trp Lys Glu Met
            170                 175                 180

CAT AAG CTT TTG CCA TTC TCA CCG GAT TCA GTC GTC ACT CAT GGT GAT      5308
His Lys Leu Leu Pro Phe Ser Pro Asp Ser Val Val Thr His Gly Asp
        185                 190                 195

TTC TCA CTT GAT AAC CTT ATT TTT GAC GAG GGG AAA TTA ATA GGT TGT      5356
Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu Gly Lys Leu Ile Gly Cys
    200                 205                 210

ATT GAT GTT GGA CGA GTC GGA ATC GCA GAC CGA TAC CAG GAT CTT GCC      5404
Ile Asp Val Gly Arg Val Gly Ile Ala Asp Arg Tyr Gln Asp Leu Ala
215                 220                 225                 230
```

```
ATC CTA TGG AAC TGC CTC GGT GAG TTT TCT CCT TCA TTA CAG AAA CGG      5452
Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser Pro Ser Leu Gln Lys Arg
                235                 240                 245

CTT TTT CAA AAA TAT GGT ATT GAT AAT CCT GAT ATG AAT AAA TTG CAG      5500
Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro Asp Met Asn Lys Leu Gln
            250                 255                 260

TTT CAT TTG ATG CTC GAT GAG TTT TTC TAA TCAGAATTGG TTAATTGGTT        5550
Phe His Leu Met Leu Asp Glu Phe Phe  *
        265                 270

GTAACACTGG CAGAGCATTA CGCTGACTTG ACGGGACGGC GGCTTTGTTG AATAAATCGA    5610

ACTTTTGCTG AGTTGAAGGA TCAGATCACG CATCTTCCCG ACAACGCAGA CCGTTCCGTG    5670

GCAAAGCAAA AGTTCAAAAT CACCAACTGG TCCACCTACA ACAAAGCTCT CATCAACCGT    5730

GGCTCCCTCA CTTTCTGGCT GGATGATGGG GCGATTCAGG CCTGGTATGA GTCAGCAACA    5790

CCTTCTTCAC GAGGCAGACC TCAGCGCCCC CCCCCCCCTG CAGGTCGA                 5838
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val Thr Leu
 1               5                  10                  15

Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly Leu Leu
            20                  25                  30

Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly Val Leu
        35                  40                  45

Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val Leu Gly
    50                  55                  60

Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala Ser Leu
65                  70                  75                  80

Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro Val Leu
                85                  90                  95

Trp Ile Leu Tyr Ala Gly Arg Ile Val Ala Gly Ile Thr Gly Ala Thr
            100                 105                 110

Gly Ala Val Ala Gly Ala Tyr Ile Ala Asp Ile Thr Asp Gly Glu Asp
        115                 120                 125

Arg Ala Arg His Phe Gly Leu Met Ser Ala Cys Phe Gly Val Gly Met
    130                 135                 140

Val Ala Gly Pro Val Ala Gly Gly Leu Leu Gly Ala Ile Ser Leu His
145                 150                 155                 160

Ala Pro Phe Leu Ala Ala Ala Val Leu Asn Gly Leu Asn Leu Leu Leu
                165                 170                 175
```

```
Gly Cys Phe Leu Met Gln Glu Ser His Lys Gly Glu Arg Arg Pro Met
                180                 185                 190

Pro Leu Arg Ala Phe Asn Pro Val Ser Ser Phe Arg Trp Ala Arg Gly
        195                 200                 205

Met Thr Ile Val Ala Ala Leu Met Thr Val Phe Phe Ile Met Gln Leu
    210                 215                 220

Val Gly Gln Val Pro Ala Ala Leu Trp Val Ile Phe Gly Glu Asp Arg
225                 230                 235                 240

Phe Arg Trp Ser Ala Thr Met Ile Gly Leu Ser Leu Ala Val Phe Gly
                245                 250                 255

Ile Leu His Ala Leu Ala Gln Ala Phe Val Thr Gly Pro Ala Thr Lys
                260                 265                 270

Arg Phe Gly Glu Lys Gln Ala Ile Ile Ala Gly Met Ala Ala Asp Ala
        275                 280                 285

Leu Gly Tyr Val Leu Leu Ala Phe Ala Thr Arg Gly Trp Met Ala Phe
    290                 295                 300

Pro Ile Met Ile Leu Leu Ala Ser Gly Gly Ile Gly Met Pro Ala Leu
305                 310                 315                 320

Gln Ala Met Leu Ser Arg Gln Val Asp Asp Asp His Gln Gly Gln Leu
                325                 330                 335

Gln Gly Ser Leu Ala Ala Leu Thr Ser Leu Thr Ser Ile Thr Gly Pro
                340                 345                 350

Leu Ile Val Thr Ala Ile Tyr Ala Ala Ser Ala Ser Thr Trp Asn Gly
        355                 360                 365

Leu Ala Trp Ile Val Gly Ala Ala Leu Tyr Leu Val Cys Leu Pro Ala
    370                 375                 380

Leu Arg Arg Gly Ala Trp Ser Arg Ala Thr Ser Thr  *
385                 390                 395
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp
  1                 5                  10                  15

His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
                20                  25                  30

Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
            35                  40                  45

Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
        50                  55                  60

Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly
65                  70                  75                  80
```

```
Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His
                  85                  90                  95

Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp
             100                 105                 110

Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly
         115                 120                 125

Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe
     130                 135                 140

Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
145                 150                 155                 160

Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
                 165                 170                 175

Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
             180                 185                 190

His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
         195                 200                 205

Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala  *
     210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn
  1               5                  10                  15

Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn
             20                  25                  30

Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp
         35                  40                  45

Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp
     50                  55                  60

Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro
 65                  70                  75                  80

Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu
                 85                  90                  95

Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu
             100                 105                 110

Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu
         115                 120                 125

Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp
     130                 135                 140

Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu
145                 150                 155                 160
```

Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu
165 170 175

Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser
180 185 190

Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu
195 200 205

Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp
210 215 220

Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser
225 230 235 240

Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro
245 250 255

Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe *
260 265 270

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Tn5 wild type outside end"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGACTCTTA TACACAAGT 19

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Tn5 mutant outside end"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTGTCTCTTA TACACATCT 19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Tn5 mutant outside end"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGTCTCTTA TACAGATCT 19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Tn5 wild type inside end"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGTCTCTTG ATCAGATCT 19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Plasmid pRZ4196"

(ix) FEATURE:
(A) NAME/KEY: repeat_unit
(B) LOCATION: 94..112
(D) OTHER INFORMATION: /note= "Wild type OE sequence"

(ix) FEATURE:
(A) NAME/KEY: repeat_unit
(B) LOCATION: 12184..12225
(D) OTHER INFORMATION: /note= "Cassette IE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTCCTGTAAC AATAGCAATA CCCCAAATAC CTAATGTAGT TCCAGCAAGC AAGCTAAAAA 60

GTAAAGCAAC AACATAACTC ACCCCTGCAT CTGCTGACTC TTATACACAA GTAGCGTCCC 120

GGGATCGGGA TCCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC 180

TTAATCGCCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA 240

CCGATCGCCC TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCTTT GCCTGGTTTC 300

CGGCACCAGA AGCGGTGCCG GAAAGCTGGC TGGAGTGCGA TCTTCCTGAG GCCGATACTG 360

TCGTCGTCCC CTCAAACTGG CAGATGCACG GTTACGATGC GCCCATCTAC ACCAACGTAA 420

CCTATCCCAT TACGGTCAAT CCGCCGTTTG TTCCCACGGA GAATCCGACG GGTTGTTACT 480

CGCTCACATT TAATGTTGAT GAAAGCTGGC TACAGGAAGG CCAGACGCGA ATTATTTTTG 540

ATGGCGTTAA CTCGGCGTTT CATCTGTGGT GCAACGGGCG CTGGGTCGGT TACGGCCAGG 600

ACAGTCGTTT GCCGTCTGAA TTTGACCTGA GCGCATTTTT ACGCGCCGGA GAAAACCGCC 660

TCGCGGTGAT GGTGCTGCGT TGGAGTGACG GCAGTTATCT GGAAGATCAG GATATGTGGC 720

GGATGAGCGG CATTTTCCGT GACGTCTCGT TGCTGCATAA ACCGACTACA CAAATCAGCG 780

ATTTCCATGT TGCCACTCGC TTTAATGATG ATTTCAGCCG CGCTGTACTG GAGGCTGAAG 840

TTCAGATGTG CGGCGAGTTG CGTGACTACC TACGGGTAAC AGTTTCTTTA TGGCAGGGTG 900

AAACGCAGGT CGCCAGCGGC ACCGCGCCTT TCGGCGGTGA AATTATCGAT GAGCGTGGTG 960
GTTATGCCGA TCGCGTCACA CTACGTCTGA ACGTCGAAAA CCCGAAACTG TGGAGCGCCG 1020
AAATCCCGAA TCTCTATCGT GCGGTGGTTG AACTGCACAC CGCCGACGGC ACGCTGATTG 1080
AAGCAGAAGC CTGCGATGTC GGTTTCCGCG AGGTGCGGAT TGAAAATGGT CTGCTGCTGC 1140
TGAACGGCAA GCCGTTGCTG ATTCGAGGCG TTAACCGTCA CGAGCATCAT CCTCTGCATG 1200
GTCAGGTCAT GGATGAGCAG ACGATGGTGC AGGATATCCT GCTGATGAAG CAGAACAACT 1260
TTAACGCCGT GCGCTGTTCG CATTATCCGA ACCATCCGCT GTGGTACACG CTGTGCGACC 1320
GCTACGGCCT GTATGTGGTG GATGAAGCCA ATATTGAAAC CCACGGCATG GTGCCAATGA 1380
ATCGTCTGAC CGATGATCCG CGCTGGCTAC CGGCGATGAG CGAACGCGTA ACGCGAATGG 1440
TGCAGCGCGA TCGTAATCAC CCGAGTGTGA TCATCTGGTC GCTGGGGAAT GAATCAGGCC 1500
ACGGCGCTAA TCACGACGCG CTGTATCGCT GGATCAAATC TGTCGATCCT TCCCGCCCGG 1560
TGCAGTATGA AGGCGGCGGA GCCGACACCA CGGCCACCGA TATTATTTGC CCGATGTACG 1620
CGCGCGTGGA TGAAGACCAG CCCTTCCCGG CTGTGCCGAA ATGGTCCATC AAAAAATGGC 1680
TTTCGCTACC TGGAGAGACG CGCCCGCTGA TCCTTTGCGA ATACGCCCAC GCGATGGGTA 1740
ACAGTCTTGG CGGTTTCGCT AAATACTGGC AGGCGTTTCG TCAGTATCCC CGTTTACAGG 1800
GCGGCTTCGT CTGGGACTGG GTGGATCAGT CGCTGATTAA ATATGATGAA AACGGCAACC 1860
CGTGGTCGGC TTACGGCGGT GATTTTGGCG ATACGCCGAA CGATCGCCAG TTCTGTATGA 1920
ACGGTCTGGT CTTTGCCGAC CGCACGCCGC ATCCAGCGCT GACGGAAGCA AAACACCAGC 1980
AGCAGTTTTT CCAGTTCCGT TTATCCGGGC AAACCATCGA AGTGACCAGC GAATACCTGT 2040
TCCGTCATAG CGATAACGAG CTCCTGCACT GGATGGTGGC GCTGGATGGT AAGCCGCTGG 2100
CAAGCGGTGA AGTGCCTCTG GATGTCGCTC CACAAGGTAA ACAGTTGATT GAACTGCCTG 2160
AACTACCGCA GCCGGAGAGC GCCGGGCAAC TCTGGCTCAC AGTACGCGTA GTGCAACCGA 2220
ACGCGACCGC ATGGTCAGAA GCCGGGCACA TCAGCGCCTG GCAGCAGTGG CGTCTGGCGG 2280
AAAACCTCAG TGTGACGCTC CCCGCCGCGT CCCACGCCAT CCCGCATCTG ACCACCAGCG 2340
AAATGGATTT TTGCATCGAG CTGGGTAATA AGCGTTGGCA ATTTAACCGC CAGTCAGGCT 2400
TTCTTTCACA GATGTGGATT GGCGATAAAA AACAACTGCT GACGCCGCTG CGCGATCAGT 2460
TCACCCGTGC ACCGCTGGAT AACGACATTG GCGTAAGTGA AGCGACCCGC ATTGACCCTA 2520
ACGCCTGGGT CGAACGCTGG AAGGCGGCGG GCCATTACCA GGCCGAAGCA GCGTTGTTGC 2580
AGTGCACGGC AGATACACTT GCTGATGCGG TGCTGATTAC GACCGCTCAC GCGTGGCAGC 2640
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TGAACTGCCA GCTGGCGCAG GTAGCAGAGC GGGTAAACTG GCTCGGATTA GGGCCGCAAG 2820
AAAACTATCC CGACCGCCTT ACTGCCGCCT GTTTTGACCG CTGGGATCTG CCATTGTCAG 2880
ACATGTATAC CCCGTACGTC TTCCCGAGCG AAAACGGTCT GCGCTGCGGG ACGCGCGAAT 2940

TGAATTATGG CCCACACCAG TGGCGCGGCG ACTTCCAGTT CAACATCAGC CGCTACAGTC 3000
AACAGCAACT GATGGAAACC AGCCATCGCC ATCTGCTGCA CGCGGAAGAA GGCACATGGC 3060
TGAATATCGA CGGTTTCCAT ATGGGGATTG GTGGCGACGA CTCCTGGAGC CCGTCAGTAT 3120
CGGCGGATTC CAGCTGAGCG CCGGTCGCTA CCATTACCAG TTGGTCTGGT GTCAAAAATA 3180
ATAATAACCG GGCAGGCCAT GTCTGCCCGT ATTTCGCGTA AGGAAATCCA TTATGTACTA 3240
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GTTAGTGATG TTTGCGCCGT TCTTTATTTT TATCTTCGGG CCACTGTTAC AATACAACAT 3540
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GCAGGAGAGA TTTCACCGCA TAGTCCCTTT TTTATCGCTG CGTTGCTAAA TATTGTCACT 8160
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ATTTTGTTGA TTATTTATTT TTCAGCGCAA TTGATAGGCC AAATTCCCGC AACGGTGTGG 8340
GTGCTATTTA CCGAAAATCG TTTTGGATGG AATAGCATGA TGGTTGGCTT TTCATTAGCG 8400
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TTAGCGTTTA TATCTGAAGG TTGGTTAGAT TTCCCTGTTT TAATTTTATT GGCTGGTGGT 8580
GGGATCGCTT TACCTGCATT ACAGGGAGTG ATGTCTATCC AAACAAAGAG TCATGAGCAA 8640
GGTGCTTTAC AGGGATTATT GGTGAGCCTT ACCAATGCAA CCGGTGTTAT TGGCCCATTA 8700
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1. A system for transposing a transposable DNA sequence *in vitro*, the system comprising:

a Tn*5* transposase modified relative to a wild type Tn*5* transposase, the modified transposase comprising a change relative to the wild type Tn*5* transposase that causes the modified transposase to bind to Tn*5* outside end repeat sequences with greater avidity than the wild type Tn*5* transposase, and a change relative to the wild type Tn*5* transposase that causes the modified transposase to be less likely than the wild type transposase to assume an inactive multimeric form;

a donor DNA molecule comprising the transposable DNA sequence, the DNA sequence being flanked at its 5'- and 3'-ends by the Tn*5* outside end repeat sequences; and

a target DNA molecule into which the transposable element can transpose.

2. A system as claimed in Claim 1 wherein the change that causes the modified transposase to bind with greater avidity is characterized as a substitution mutation at position 54 of the wild type transposase.

3. A system as claimed in Claim 2 wherein position 54 is a lysine.

4. A system as claimed in Claim 1 wherein the change that causes the modified transposase to be less likely to assume an inactive multimeric form is characterized as a substitution mutation at position 372 of the wild type transposase.

5. A system as claimed in Claim 4 wherein position 372 is a proline.

6. A system as claimed in Claim 1 wherein the modified transposase further comprises a substitution mutation at position 56 of the wild type transposase.

7. A system as claimed in Claim 6 wherein position 56 is an alanine.

8. A system as claimed in Claim 1 wherein the donor DNA molecule is flanked at its 5'- and 3'-ends by an 18 or 19 base pair flanking DNA sequence comprising nucleotide A at position 10, nucleotide T at position 11, and nucleotide A at position 12.

9. The system as claimed in Claim 8 wherein the flanking sequence further comprises a nucleotide at position 4 selected from the group consisting of A or T.

10. The system as claimed in Claim 8 wherein the flanking sequence further comprises a nucleotide at position 15 selected from the group consisting of G or C.

11. The system as claimed in Claim 8 wherein the flanking sequence further comprises a nucleotide at position 17 selected from the group consisting of A or T.

12. The system as claimed in Claim 8 wherein the flanking sequence further comprises a nucleotide at position 18 selected from the group consisting of G or C.

13. The system as claimed in Claim 8 wherein the flanking sequence has the sequence 5'-CTGTCTCTTATACACATCT-3'.

14. The system as claimed in Claim 8 wherein the flanking sequence has the sequence 5'-CTGTCTCTTATACAGATCT-3'.

15. A Tn5 transposase modified relative to a wild type Tn5 transposase, the modified transposase comprising:

a change relative to the wild type Tn5 transposase that causes the modified transposase to bind to Tn5 outside end repeat sequences of a donor DNA with greater avidity than the wild type Tn5 transposase; and

a change relative to the wild type Tn5 transposase that causes the modified transposase to be less likely than the wild type transposase to assume an inactive multimeric form.

16. A modified Tn5 transposase as claimed in Claim 15 wherein the change that causes the modified transposase to bind with greater avidity is characterized as a substitution mutation at position 54 of the wild type transposase.

17. A modified Tn5 transposase as claimed in Claim 16 wherein position 54 is a lysine.

18. A modified Tn5 transposase as claimed in Claim 15 wherein the change that causes the modified transposase to be less likely to assume an inactive multimeric form is characterized as a substitution mutation at position 372 of the wild type transposase.

19. A modified Tn5 transposase as claimed in Claim 18 wherein position 372 is a proline.

20. A modified Tn5 transposase as claimed in Claim 15 further comprising a substitution mutation at position 56 of the wild type transposase.

21. A modified Tn5 transposase as claimed in Claim 20 wherein position 56 is alanine.

22. A genetic construct comprising a nucleotide sequence that can encode a Tn5 transposase that both has greater avidity for Tn5 outside end repeats and is less likely to assume an inactive multimeric form than a wild type Tn5 transposase.

23. A genetic construct as claimed in Claim 22 comprising a nucleotide sequence that encodes a lysine residue at amino acid 54 of the transposase.

24. A genetic construct as claimed in Claim 22 comprising a nucleotide sequence that encodes a proline residue at amino acid 372 of the transposase.

25. A genetic construct as claimed in Claim 22 comprising a nucleotide sequence that encodes a lysine residue at amino acid 54 of the transposase and a proline residue at amino acid 372 of the transposase.

26. A genetic construct as claimed in Claim 22 comprising the nucleotide sequence of SEQ ID NO:1.

27. A genetic construct comprising:

a transposable DNA sequence flanked at its 5' and 3' ends by an 18 or 19 base pair flanking DNA sequence comprising nucleotide A at position 10, nucleotide T at position 11, and nucleotide A at position 12.

28. The construct of Claim 27 further comprising, at position 4 of the flanking sequence, a nucleotide selected from the group consisting of T or A.

29. The construct of Claim 27 further comprising, at position 15 of the flanking sequence, a nucleotide selected from the group consisting of G or C.

30. The construct of Claim 27 further comprising, at position 17 of the flanking sequence, a nucleotide selected from the group consisting of T or A.

31. The construct of Claim 27 further comprising, at position 18 of the flanking sequence, a nucleotide selected from the group consisting of G or C.

32. The construct as claimed in Claim 27 wherein the flanking sequence has the sequence 5'-CTGTCTCTTATACACATCT-3'.

33. The construct as claimed in Claim 27 wherein the flanking sequence has the sequence 5'-CTGTCTCTTATACAGATCT-3'.

34. A method for *in vitro* transposition, the method comprising the steps of:

combining a donor DNA molecule that comprises a transposable DNA sequence of interest, the DNA sequence of interest being flanked at its 5'- and 3'-ends by Tn5 outside end repeat sequences, with a target DNA molecule and a Tn5 transposase modified relative to wild type Tn5 transposase in a suitable reaction buffer at a temperature below a physiological temperature until the modified transposase binds to the outside end repeat sequences; and

raising the temperature to a physiological temperature for a period of time sufficient for the enzyme to catalyze *in vitro* transposition,

wherein the modified transposase comprises a change relative to the wild type Tn5 transposase that causes the modified transposase to bind to the Tn5 outside end repeat sequences with greater avidity than the wild type Tn5 transposase, and a change relative to the wild type Tn5 transposase that causes the modified transposase to be less likely than the wild type transposase to assume an inactive multimeric form.

35. A method as claimed in Claim 34 wherein the change that causes the modified transposase to bind with greater avidity is characterized as a substitution mutation at position 54 of the wild type transposase.

36. A method as claimed in Claim 35 wherein position 54 is a lysine.

37. A method as claimed in Claim 34 wherein the change that causes the modified transposase to be less likely to assume an inactive multimeric form is characterized as a substitution mutation at position 372 of the wild type transposase.

38. A method as claimed in Claim 37 wherein position 372 is a proline.

39. A method as claimed in Claim 34 wherein the modified transposase further comprises a substitution mutation at position 56 of the wild type transposase.

40. A method as claimed in Claim 39 wherein position 56 is an alanine.

41. A method as claimed in Claim 34 wherein the DNA sequence of interest is flanked at its 5'- and 3'-ends by an 18 or 19 base pair flanking DNA sequence comprising nucleotide A at position 10, nucleotide T at position 11, and nucleotide A at position 12.

42. The method as claimed in Claim 41 wherein the flanking sequence further comprises a nucleotide at position 4 selected from the group consisting of A or T.

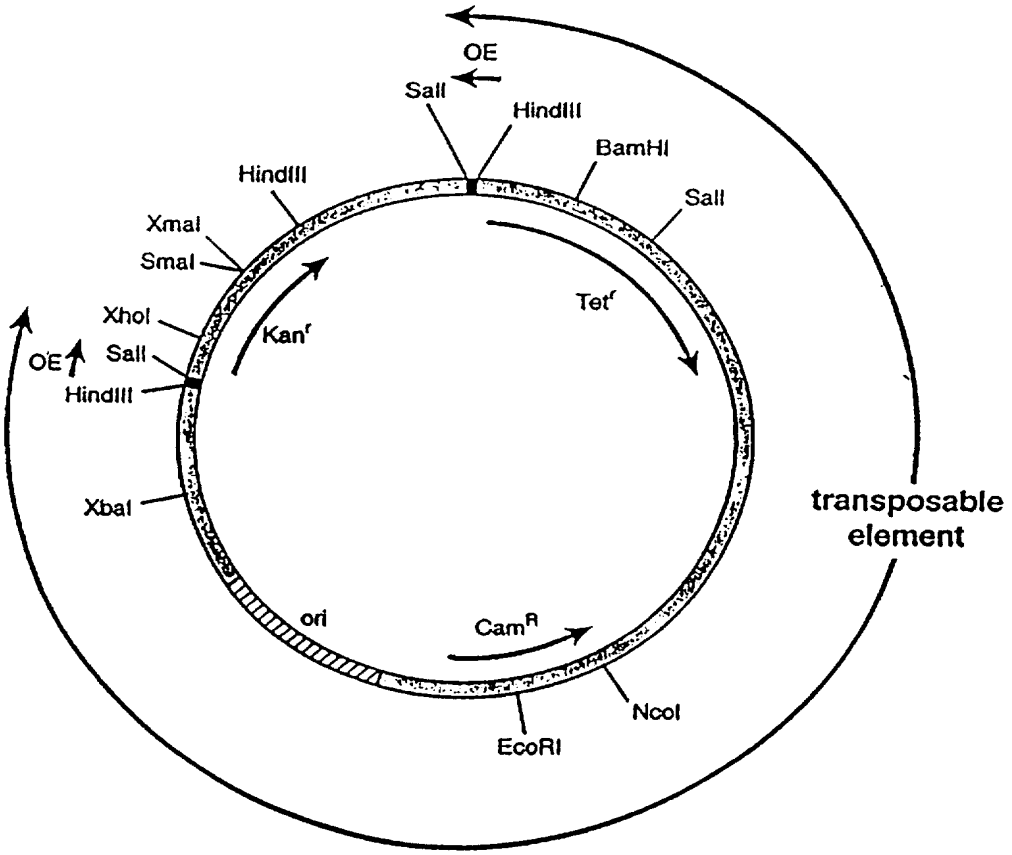
43. The method as claimed in Claim 41 wherein the flanking sequence further comprises a nucleotide at position 15 selected from the group consisting of G or C.

44. The method as claimed in Claim 41 wherein the flanking sequence further comprises a nucleotide at position 17 selected from the group consisting of A or T.

45. The method as claimed in Claim 41 wherein the flanking sequence further comprises a nucleotide at position 18 selected from the group consisting of G or C.

46. The method as claimed in Claim 41 wherein the flanking sequence has the sequence 5'-CTGTCTCTTATACACATCT-3'.

47. The method as claimed in Claim 41 wherein the flanking sequence has the sequence 5'-CTGTCTCTTATACAGATCT-3'.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SalI
HindIII
BamHI
SalI
HindIII
XmaI
SmaI
XhoI
SalI
HindIII
OE
Kan^r
Tet^r
XbaI
ori
Cam^R
NcoI
EcoRI
transposable element

FIG 1

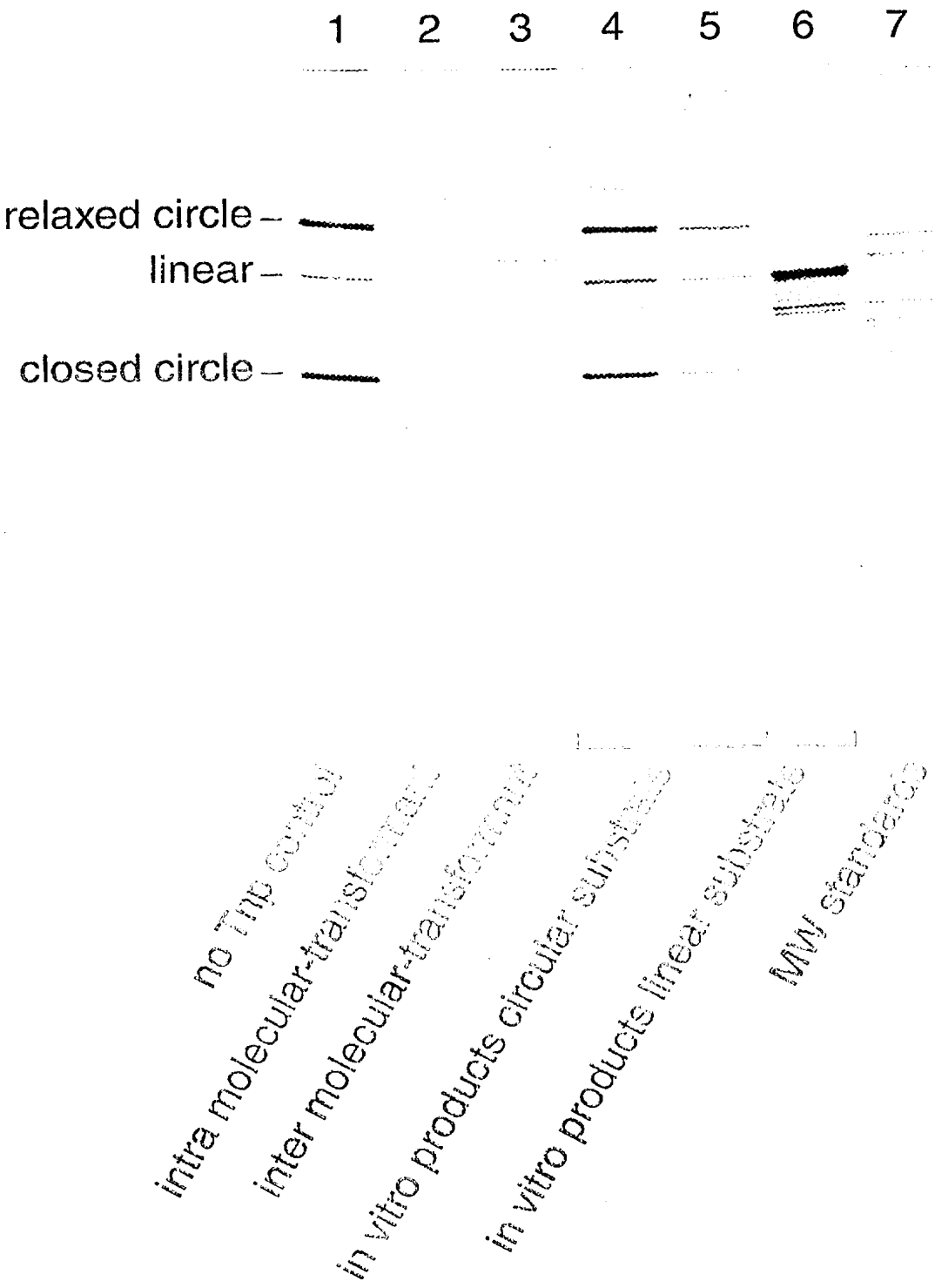

FIG 2
SUBSTITUTE SHEET (RULE 26)

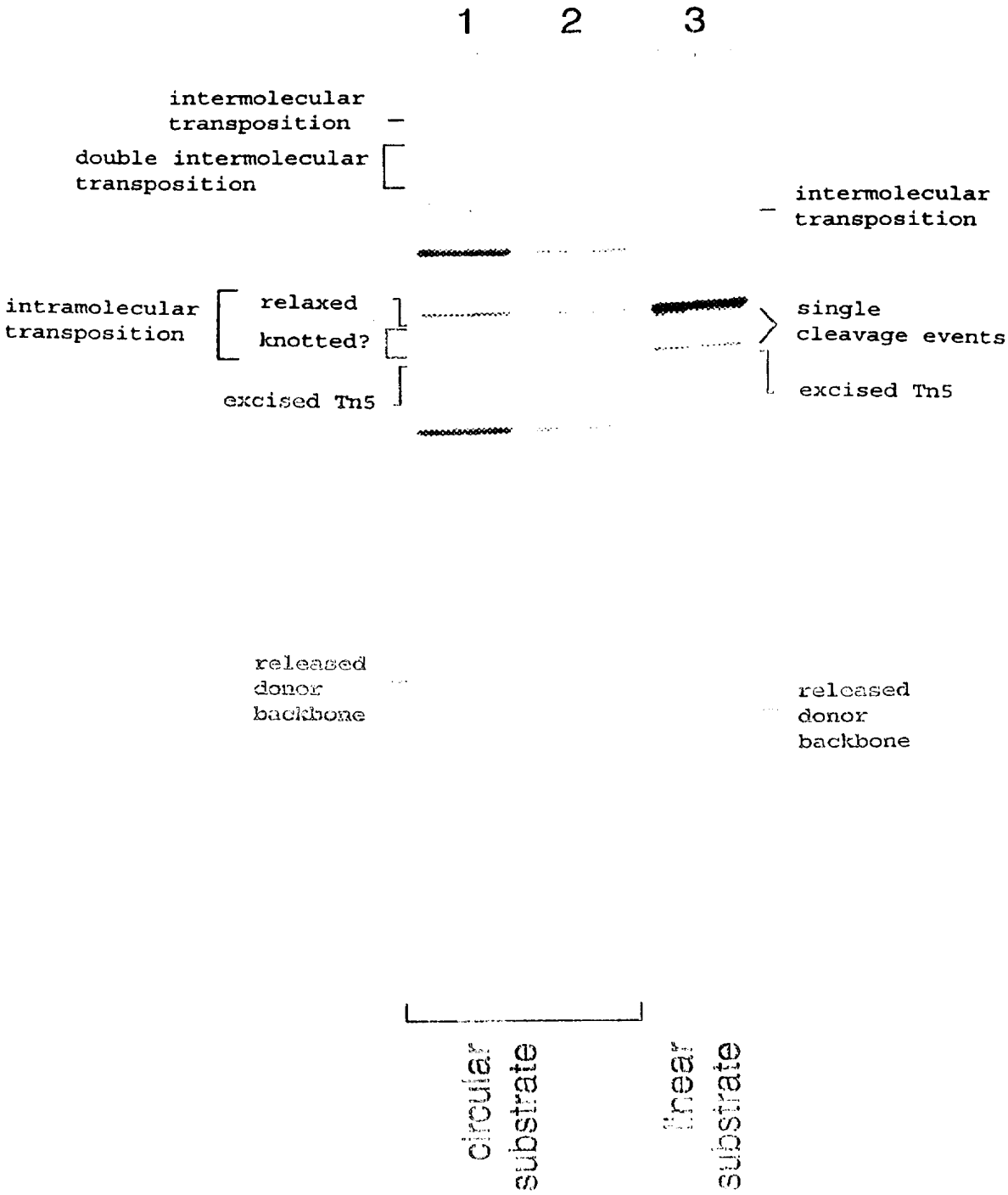

FIG 3

SUBSTITUTE SHEET (RULE 26)

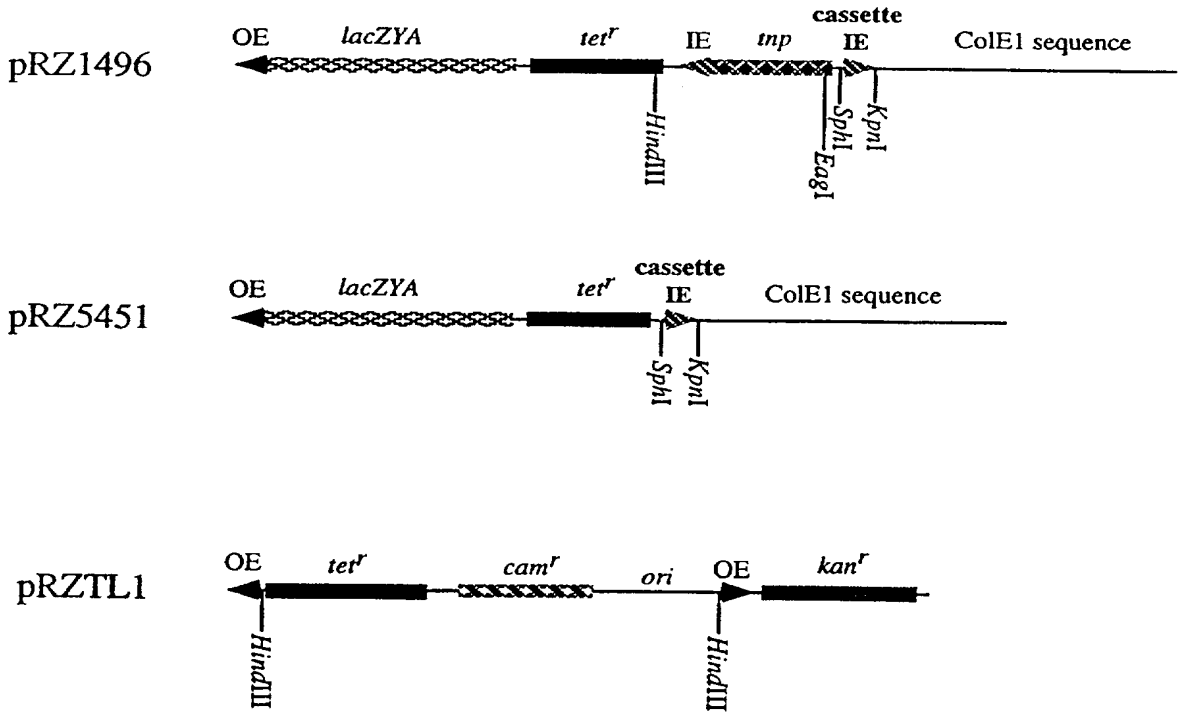
pRZ1496
OE
lacZYA
tet^r
IE
tnp
cassette
IE
ColE1 sequence
HindIII
SphI
EagI
KpnI
pRZ5451
OE
lacZYA
tet^r
cassette
IE
ColE1 sequence
SphI
KpnI
pRZTL1
OE
tet^r
cam^r
ori
OE
kan^r
HindIII
HindIII

FIG 4

a

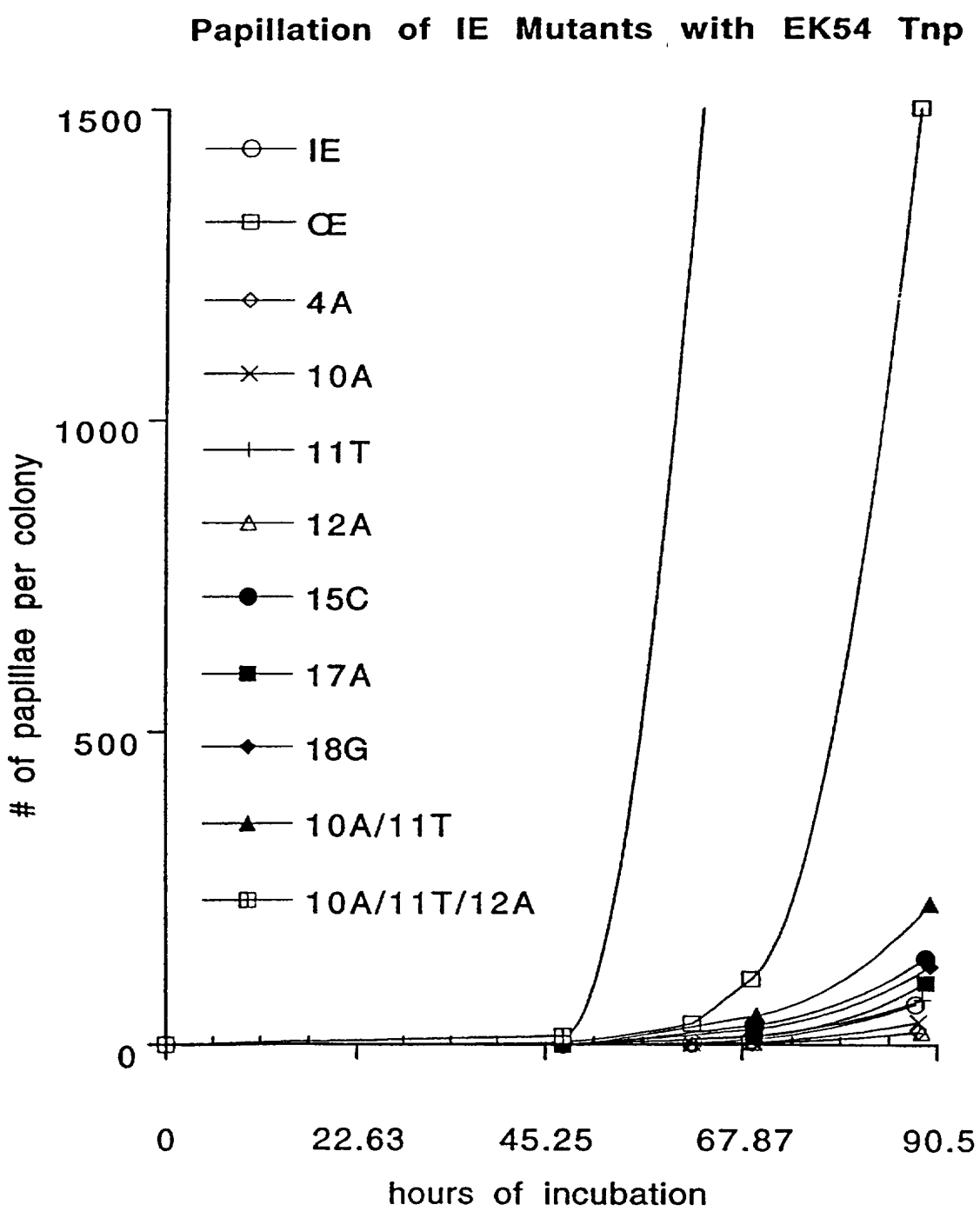
Papillation of IE Mutants with EK54 Tnp
1500
1000
500
0
# of papillae per colony
IE
CE
4A
10A
11T
12A
15C
17A
18G
10A/11T
10A/11T/12A
0
22.63
45.25
67.87
90.5
hours of incubation

FIG 5

b

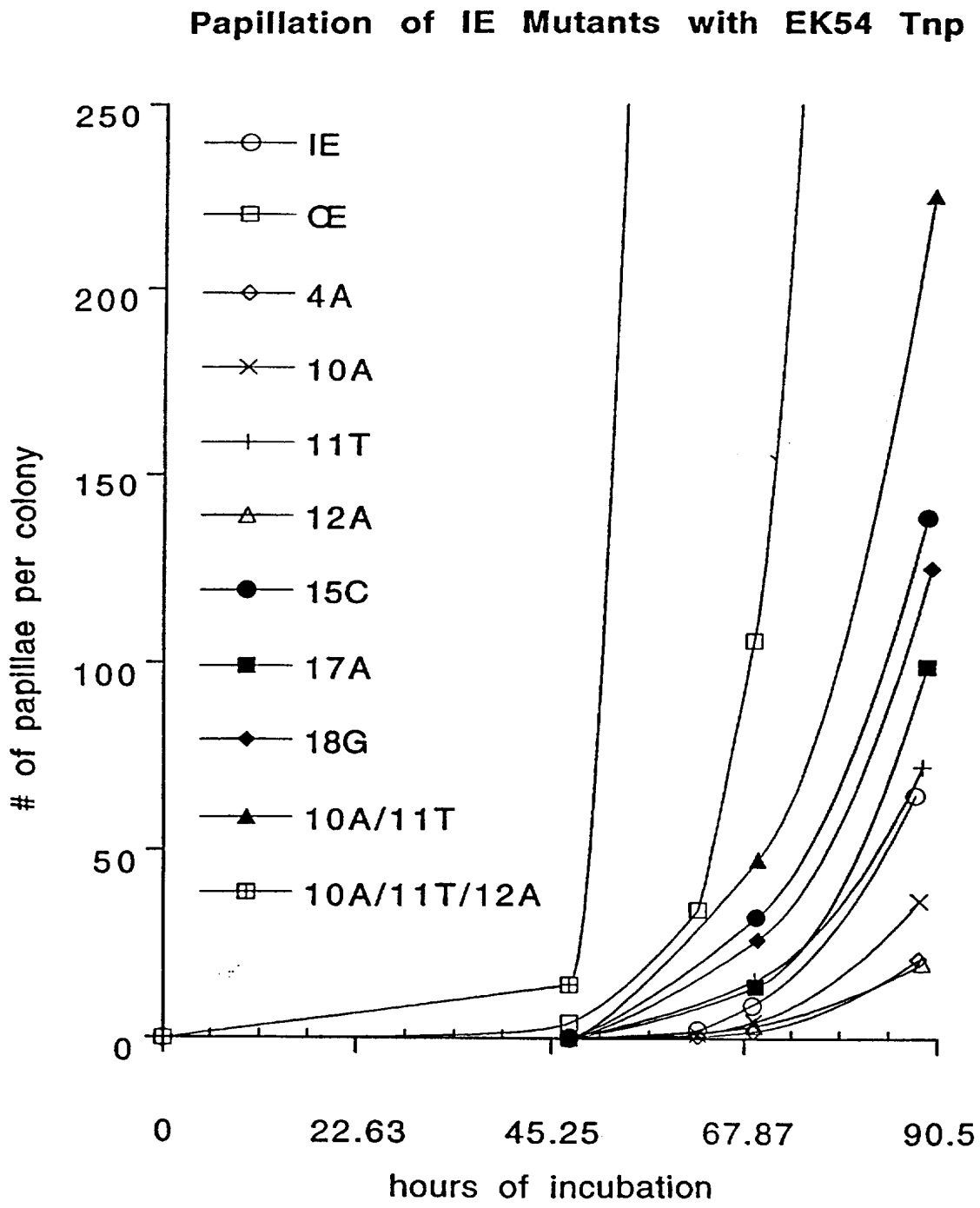
Papillation of IE Mutants with EK54 Tnp
250
200
150
100
50
0
# of papillae per colony
IE
CE
4A
10A
11T
12A
15C
17A
18G
10A/11T
10A/11T/12A
0
22.63
45.25
67.87
90.5
hours of incubation

FIG 6

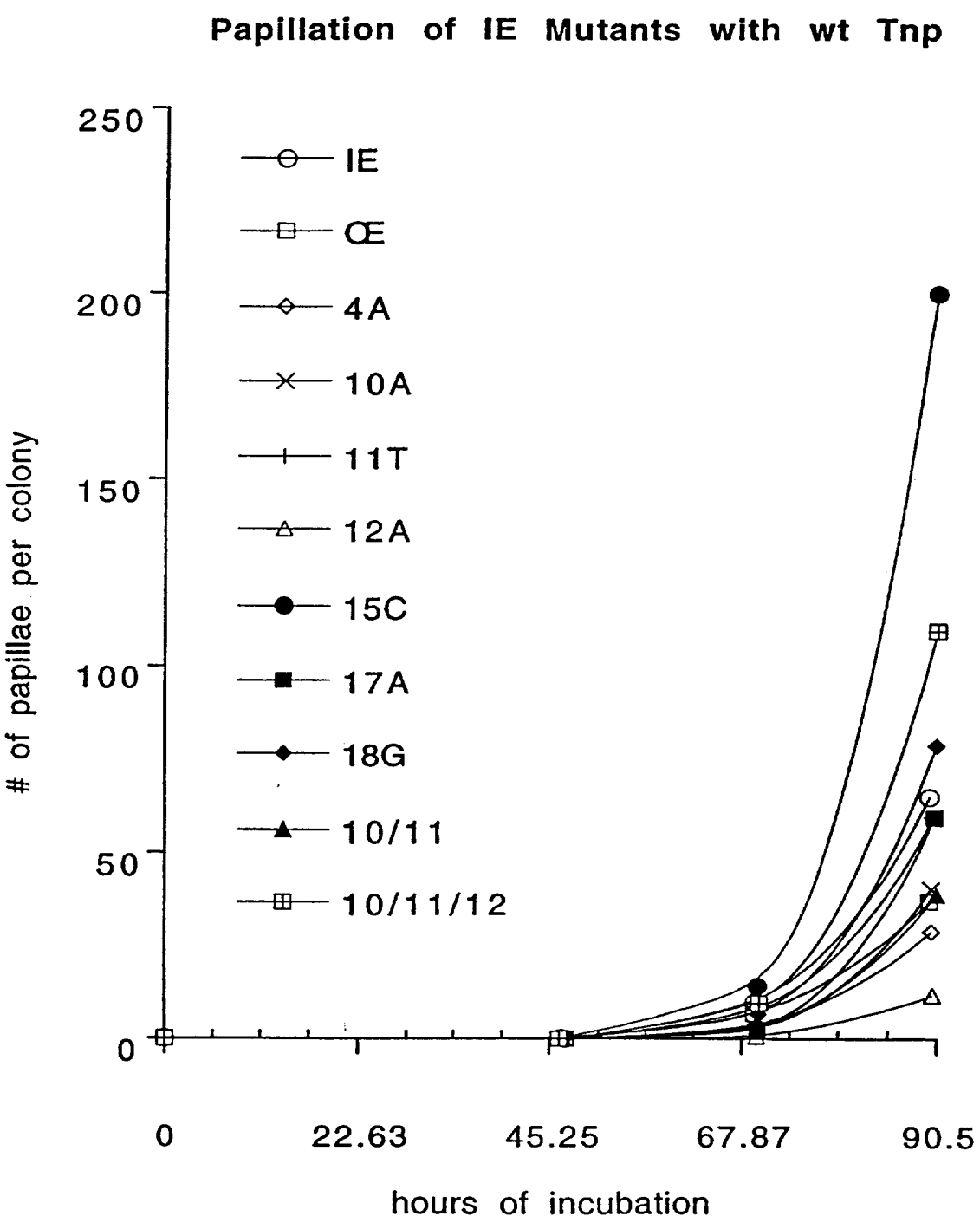
Papillation of IE Mutants with wt Tnp
250
200
150
100
50
0
# of papillae per colony
IE
ŒE
4A
10A
11T
12A
15C
17A
18G
10/11
10/11/12
0
22.63
45.25
67.87
90.5
hours of incubation

FIG 7

a

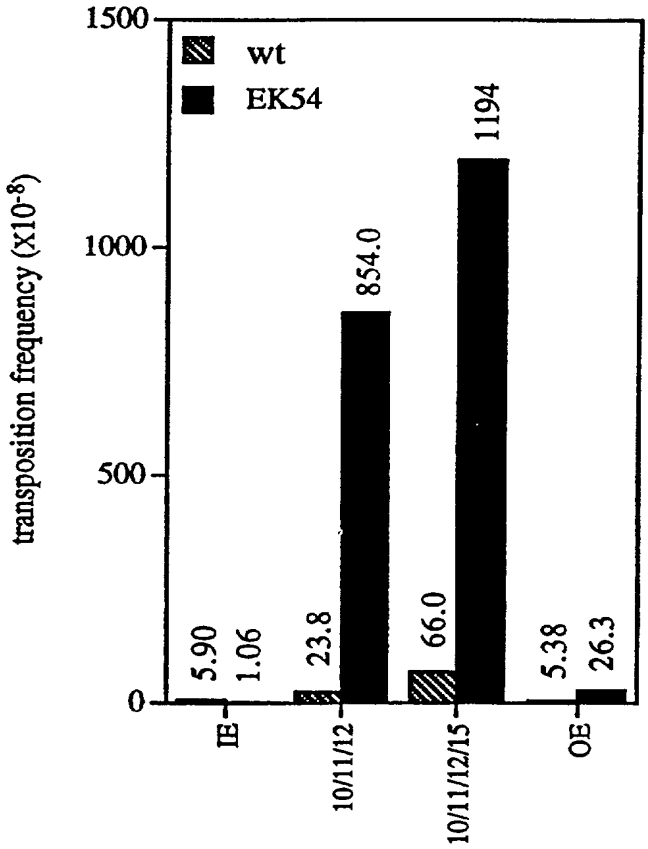
1500
1000
500
0
transposition frequency (X10-8)
wt
EK54
5.90
1.06
23.8
854.0
66.0
1194
5.38
26.3
IE
10/11/12
10/11/12/15
OE

FIG 8

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/15941

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/55 C12N9/22 C12N15/90 C12N15/85

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ZHOU M ET AL: "Three types of novel mutations in the NH-2-terminus of Tn5 transposase: Structure-function of transposase." KEYSTONE SYMPOSIUM ON TRANSPOSITION AND SITE-SPECIFIC RECOMBINATION: MECHANISM AND BIOLOGY, PARK CITY, UTAH, USA, JANUARY 21-28, 1994. JOURNAL OF CELLULAR BIOCHEMISTRY SUPPLEMENT 0 (18B). 1994. 45. ISSN: 0733-1959, XP002052633 see the whole document --- -/--	1-3, 15-17, 22,23, 26,34-36

[X] Further documents are listed in the continuation of box C

[ ] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

1

Date of the actual completion of the international search	Date of mailing of the international search report
20 January 1998	03/02/1998

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx 31 651 epo nl, Fax: (+31-70) 340-3016	Hix, R

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/15941

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	WEINREICH M D ET AL: "Evidence that the cis preference of the Tn5 transposase is caused by nonproductive multimerization." GENES & DEVELOPMENT 8 (19). 1994. 2363-2374. ISSN: 0890-9369, XP002052634 cited in the application see the whole document	1,4,5, 15,18, 19,22, 24,26, 34,37,38
Y	DELONG, ALISON ET AL: "Trans-acting transposase mutant from Tn5" PROC. NATL. ACAD. SCI. U. S. A. (1991), 88(14), 6072-6 CODEN: PNASA6;ISSN: 0027-8424, 1991, XP002052635 see the whole document	1-47
Y	WIEGAND, TORSTEN W. ET AL: "Characterization of two hypertransposing Tn5 mutants" J. BACTERIOL. (1992), 174(4), 1229-39 CODEN: JOBAAY;ISSN: 0021-9193, February 1992, XP002052636 see the whole document	1-47
Y	WIEGAND, TORSTEN WALTER: "Transposase mutants that increase the transposition frequency of Tn5" (1993) 164 PP. AVAIL.: UNIV. MICROFILMS INT., ORDER NO. DA9315014 FROM: DISS. ABSTR. INT. B 1993, 54(6), 2886, 1993, XP002052637 see the whole document	1-47
Y	WEINREICH M D ET AL: "A functional analysis of the Tn5 transposase. Identification of domains required for DNA binding and multimerization." J. MOL. BIOL., vol. 241, 1993, pages 166-177, XP002052638 see the whole document	1-47
Y	JILK R A ET AL: "The organization of the outside end of transposon Tn5." JOURNAL OF BACTERIOLOGY, vol. 178, no. 6, March 1996, pages 1671-1679, XP002052640 see the whole document	1-47

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/15941

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
Y	R.C. JOHNSON ET AL.: "DNA sequences at the ends of transposon Tn5 required for transposition." NATURE, vol. 304, 21 July 1983, pages 280-282, XP002052641 cited in the application see the whole document	1-47
P,Y	YORK, DONA ET AL: "Purification and biochemical analyses of a monomeric form of Tn5 transposase" NUCLEIC ACIDS RES. (1996), 24(19), 3790-3796 CODEN: NARHAD;ISSN: 0305-1048, 1996, XP002052642 see the whole document	1-47
P,X	ZHOU M ET AL: "Tn5 transposase mutants that alter DNA binding specificity." JOURNAL OF MOLECULAR BIOLOGY 271 (3). 1997. 362-373. ISSN: 0022-2836, XP002052643 see the whole document	1-47
P,X	YORK, DONA ET AL: "DNA binding and phasing analyses of Tn5 transposase and a monomeric variant" NUCLEIC ACIDS RES. (1997), 25(11), 2153-2160 CODEN: NARHAD;ISSN: 0305-1048, 1997, XP002052645 see the whole document	1-47

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